

Fig.1.

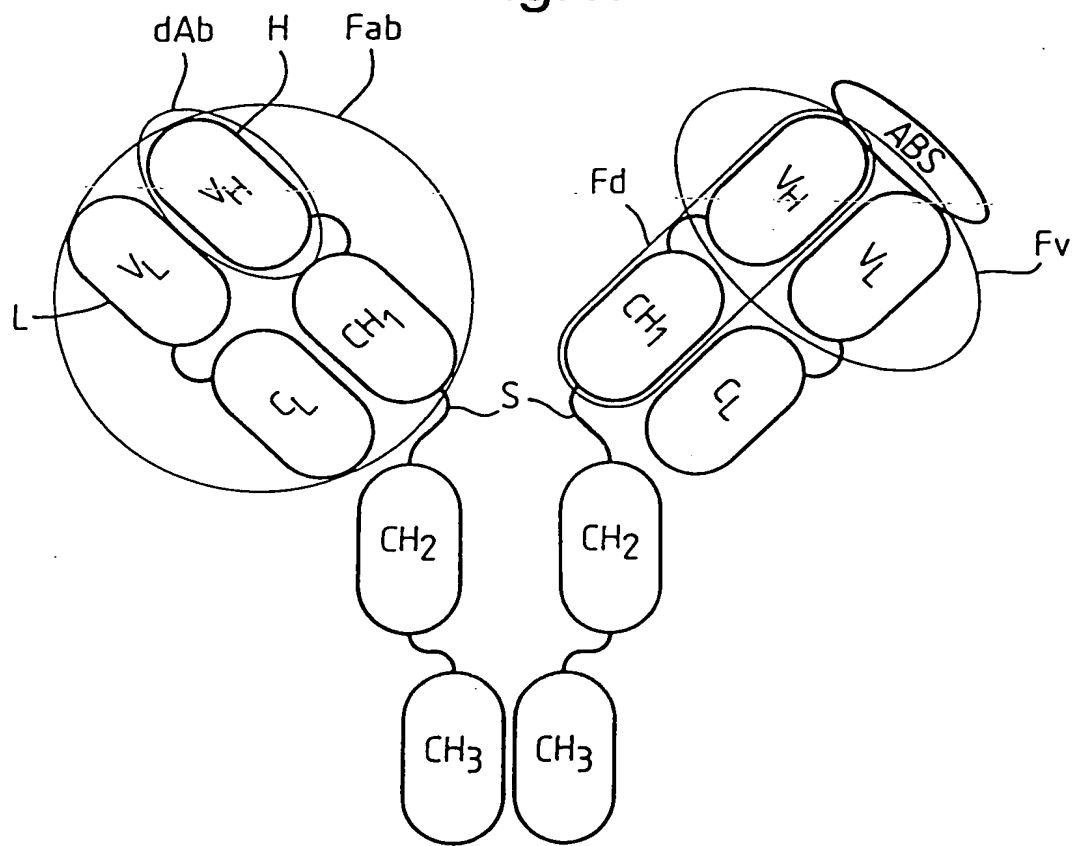


Fig. 2a

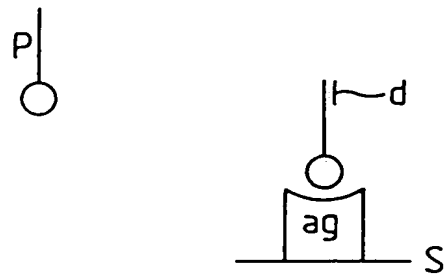


Fig. 2b

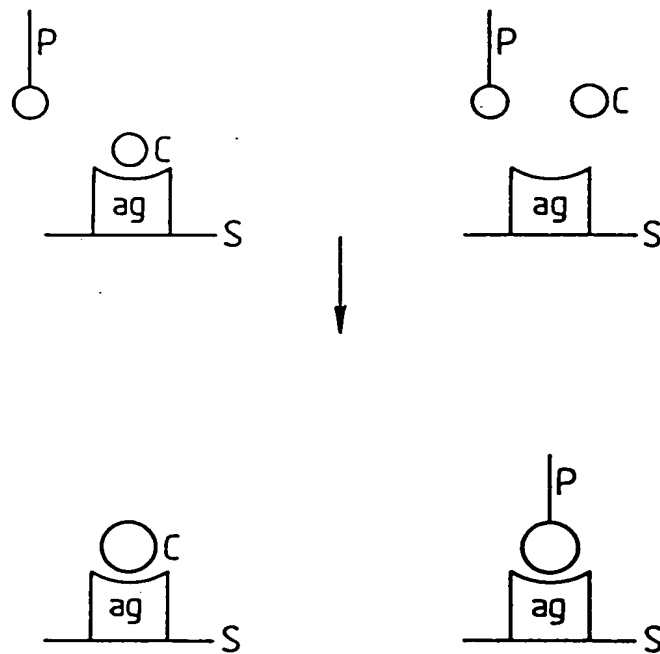
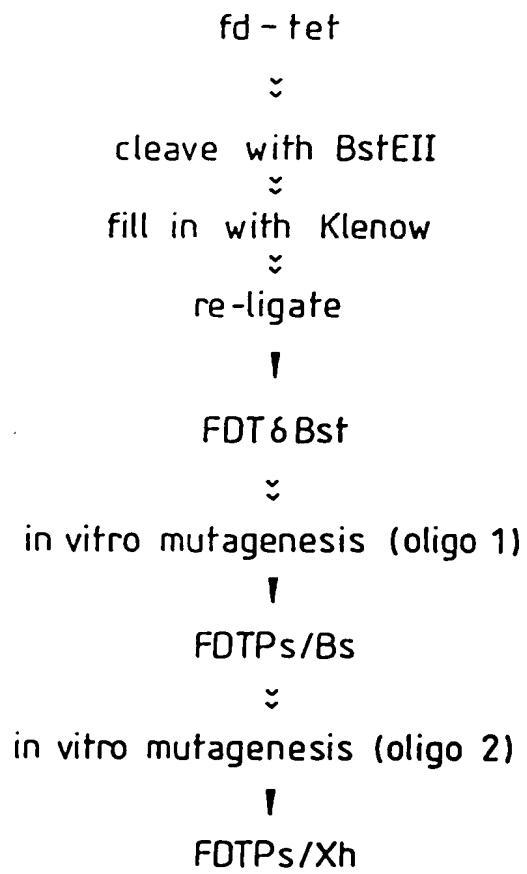
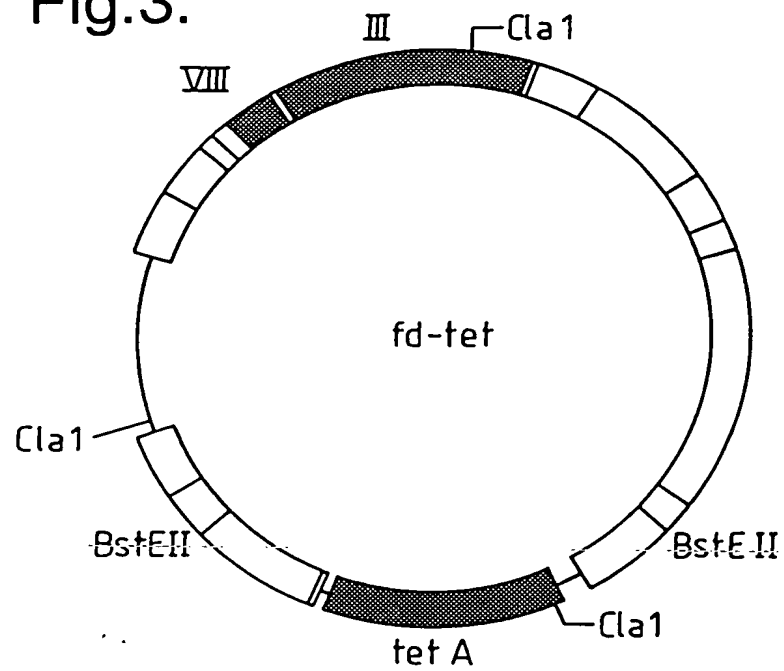


Fig.3.



<p>(1653) Oligo 1 ACA ACT TTC AAC AGT TGA GGA GAC GGT GAC CGT AAG CTT CTG CAG TTG GAC CTG AGC (SEQ ID NO. 177) GGA GTG AGA ATA (1620)</p>	<p>(1653) Oligo 2 ACA ACT TTC AAC AGT TTC CCG TTT GAT CTC GAG CTC CTG CAG TTG GAC CTG (SEQ ID NO. 178) (1704) Oligo 3 GTC GTC TTT CCA GAC GTT AGT (SEQ ID NO. 179)</p>
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Fig. 4a

<p>GENE III</p> <p>(1624) A TCT CAC TCC GCT</p>	<p>GENE III</p> <p>(1650) GAA ACTGTT GAA AGT (SEQ ID NO. 180)</p>
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<p>SIGNAL CLEAVAGE SITE</p>	<p>Q V Q L Q (SEQ ID NO. 1) V T V S S (SEQ ID NO. 2)</p>
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<p>B TCT CAC TCC GCT CAG GTC CAA CTG CAG AAG CTT ACG GTC ACC GTC TCC TCA ACT GTT GAA AGT (SEQ ID NO. 181)</p>	<p>PstI BstEII</p>
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<p>C TCT CAC TCC GCT CAG GTC CAA CTG CAG GAG CTC GAG ATC AAA CGG GAA ACT GTT GAA AGT (SEQ ID NO. 182)</p>	<p>Q V Q L Q (SEQ ID NO. 1) L E I K R (SEQ ID NO. 3)</p>
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<p>PstI XhoI</p>

Fig. 4b

Fig. 5a

rbs M K Y L L P T A A
 GCATGCAAATTCCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60
 SphI
 pelB leader
 A G L L L L A A O P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120
 PstI
 G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180
 S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAAACTGGGTTCCGCGCCTCCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240
 VHD1.3
 L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTGTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300
 S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACCTCCAAGAGCCAGTTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360
 D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420
 Linker Peptide
 Q G T T V T V S S G G G G S G G G S G
 CAAGGCACCAACGGTCAACGCTCTCCTCAGgtggaggcggttcaggcgagggtggctctggc
 430 440 450 460 470 480
 BstEII
 G G G S D I E L T Q S P A S L S A S V G
 ggtggcggatcgGACATCGAGCTCACTCAGTCTCCAGCCTCCCTTTCTGCGTCTGTGGGA
 490 500 510 520 530 540
 SacI

Fig. 5b

E T V T I T C R A S G N I H N Y L A W Y
GAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTAT
550 560 570 580 590 600

Q Q K Q G K S P Q L L V Y Y T T T L A D
CAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATTATACACAACCTTAGCAGAT
610 620 630 640 650 660

VKD1.3

G V P S R F S G S G S G T Q Y S L K I N
GGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
670 680 690 700 710 720

S L Q P E D F G S Y Y C Q H F W S T P R
AGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCTCGG
730 740 750 760 770 780

Myc Tag (TAG1)

T F G G G T K L E I K R E O K L I S E E
ACGTTCCGGTGGAGGGACCAAGCTCGAGATCAAACGGGAACAAAACTCATCTCAGAAGAG
790 800 810 820 830 840

XhoI

D L N * * (SEQ ID NO. 183)

GATCTGAATTAATAATGATCAAACGGTAATAAGGATCCAGCTCGAATTC (SEQ ID NO. 184)
850 860 870 880

EcoRI

Fig.6.

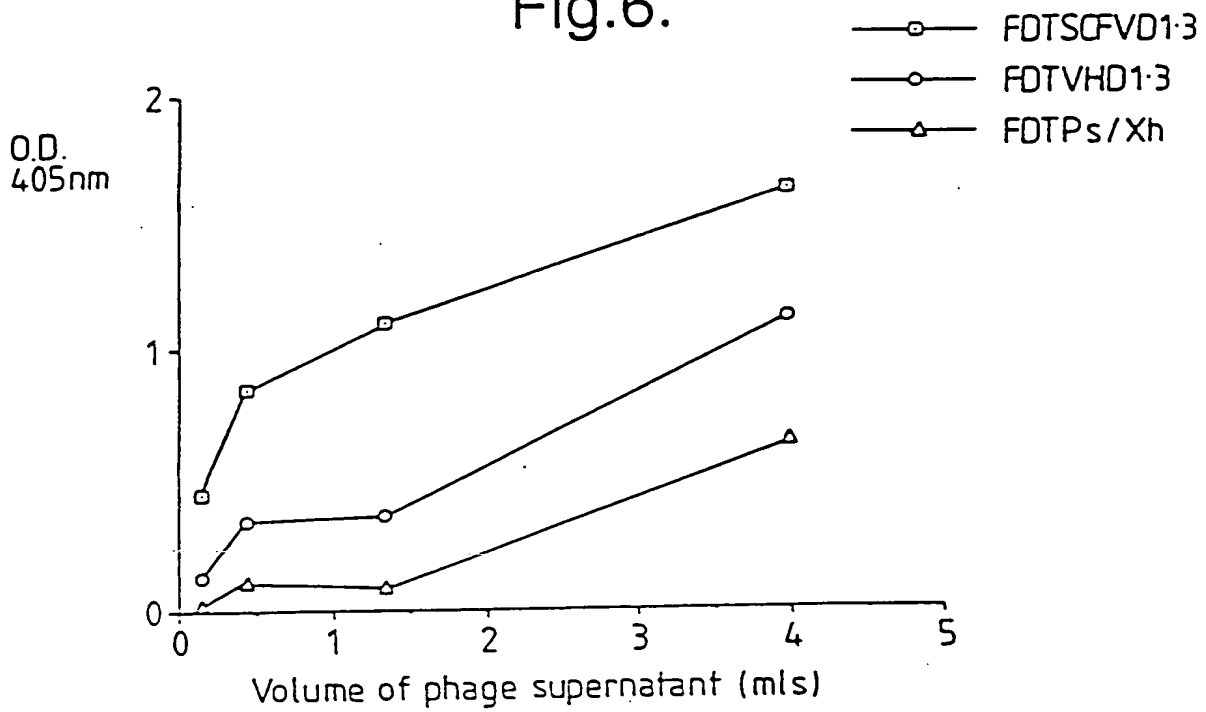


Fig.7.

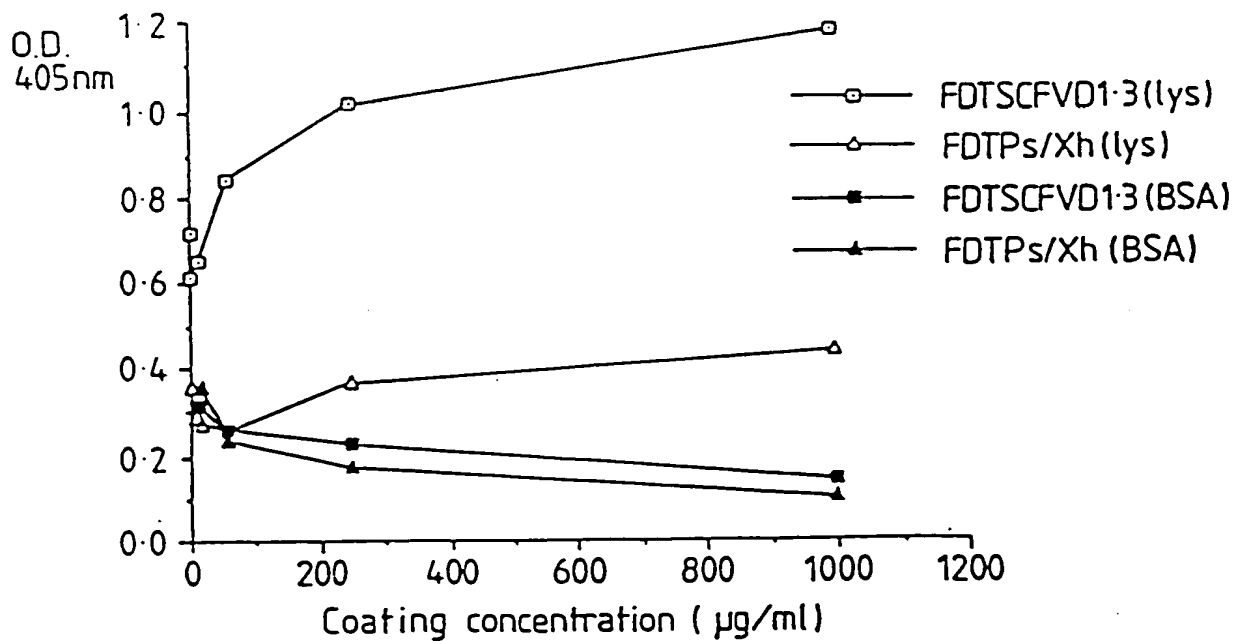


Fig.8.

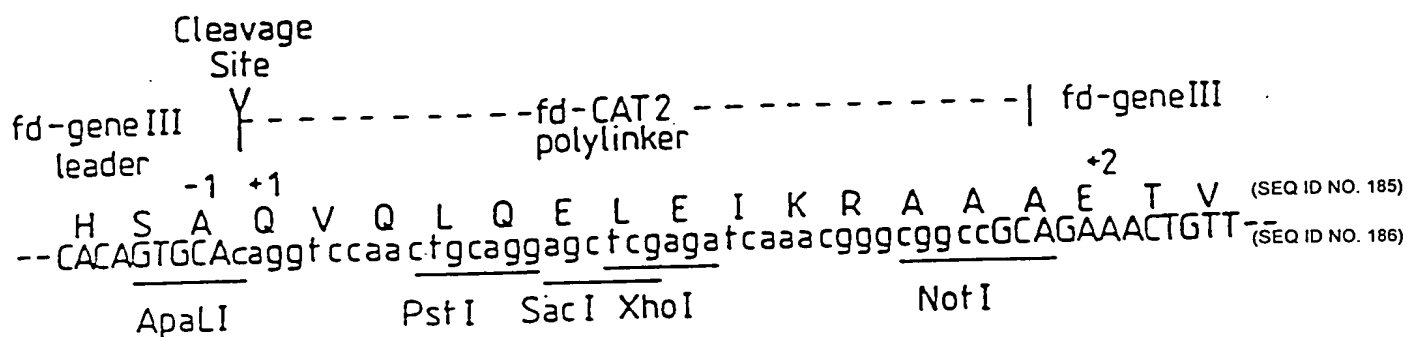


Fig.9.

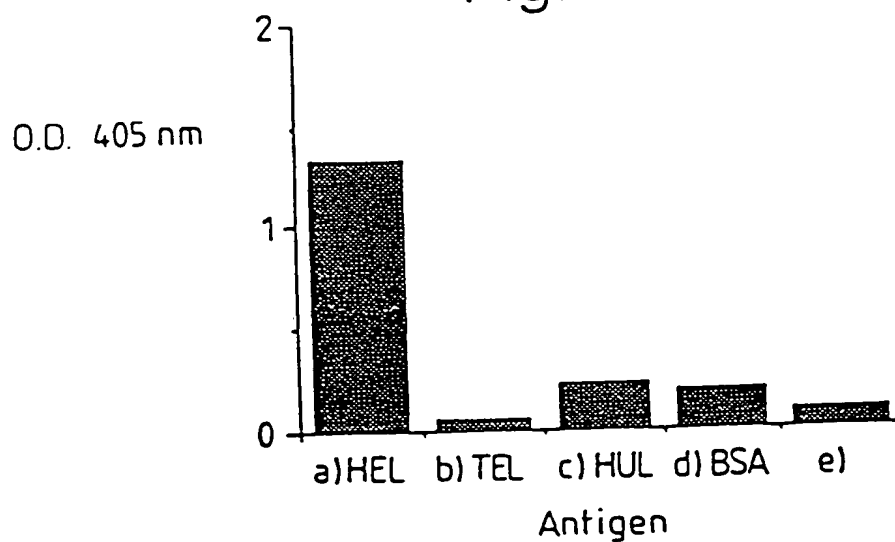


Fig. 10a

M K Y L L P T A A
GCATGCAAATTCTATTTCAGGAGACAGTCATAATGAAATACCTATTGGOCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTGCTGCCCCAACCAGCGATGGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGGCTGGTGGGGGCTCAGAGAGCTGTCCATCACATGCAACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAAACGGCTATGGTGTAAACTGGGTTGCCCAGGCTCCAGGAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTTCAGCTCTCAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAGTTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S A S T K G P S V F P L
CAAGGCACCAAGGTCAACCGTCTCTCTCAGCCTCCACCAAGGGCCCATGGGTCTTCCCCCTG
430 440 450 460 470 480

A P S S K S T S G G T A A L G C L V K D
GCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
490 500 510 520 530 540

Fig. 10b

Y F P E P V T V S W N S G A L T S G V H
TACTTCCCCGAACCGGTGAACGGTGTCTGTGGAACTCAGGGGCCCTGACCCAGGGGGGTGCAC
550 560 570 580 590 600

T F P A V L Q S S G L Y S L S S V V T V
ACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGTG
610 620 630 640 650 660

P S S S L G T Q T Y I C N V N H K P S N
CCCTCCAGTAGCTTGGGCACCCAGACCTACATCTGTCAACGTGAATCACAAGCCCCAGCAAC
670 680 690 700 710 720

T K V D K K V E P K S S * * (SEQ ID NO. 187)
ACCAAGGTTCGACACAGAAAGTTCAGCCCAATCTTCATAATAACCCGGGAGCTTGCATGCA
730 740 750 760 770 780

M K Y L L P T A A A G L
AATTCTATTTCAGGAGACAGTCTATGAATACTTATGCTACGGCAGCGCTGGAT
790 800 810 820 830 840

L L L A A Q P A M A D I E L T Q S P A S
TGTTTATTACTGTGCTGCCCCAACCCAGCATGGCCGACATCGAGCTCACCAGTCTCCAGCCT
850 860 870 880 890 900

L S A S V G E T V T I T C R A S G N I H
CCCTTCTGTGGTCTGTGGGAGAACTGTACCATCACATGTTCAGCAAGTGGGAATATTC
910 920 930 940 950 960

N Y L A W Y Q Q K Q G K S P Q L L V Y Y
ACAATTATTTAGCATGGTATCAGCAGAAACAGCGAAATCTCTCTAGCTCCCTGGTCTATT
970 980 990 1000 1010 1020

Fig. 10c

T T T L A D G V P S R F S G S G S G T Q
ATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACAC
1030 1040 1050 1060 1070 1080

Y S L K I N S L Q P E D F G S Y Y C Q H
AATATTCTCTCAAGATCAACAGCCTGCGCCTGAAGATTTTGGGAGTTATTACTGTCAAC
1090 1100 1110 1120 1130 1140

F W S T P R T F G G G T K L E I K R T V
ATTTTGGAGTACTCCTCGGACGTTGGTGGAGGCACCAAGCTCGAGATCAAACGGACTG
1150 1160 1170 1180 1190 1200

A A P S V F I F P P S D E Q L K S G T A
TGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTG
1210 1220 1230 1240 1250 1260

S V V C L L N N F Y P R E A K V Q W K V
CCTCTGTGTGTGTGCCGTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAG
1270 1280 1290 1300 1310 1320

D N A L Q S G N S Q E S V T E Q D S K D
TGGATAACGCCCTCCCAATCGGGTAACTCCCAGGAGAGTGTCAACAGAGCAGGACAGCAAGG
1330 1340 1350 1360 1370 1380

S T Y S L S S T L T L S K A D Y E K H K
ACAGCACCTACAGCCTCAGCAGCAACCTGACGCTGAGCAAAGCAGACTACGAGAAACACA
1390 1400 1410 1420 1430 1440

V Y A C E V T H Q G L S S P V T K S F N
AAGTCTACGCCCTGCGAAGTCAACCATCAGGGCCTGAGCTGCGCCGTCAAAAGAGCTTCA
1450 1460 1470 1480 1490 1500

R G E S * * (SEQ ID NO. 188)
ACCGGGGAGAGTCATAGTAAGAATTC (SEQ ID NO. 189)
1510 1520

Fig. 10d

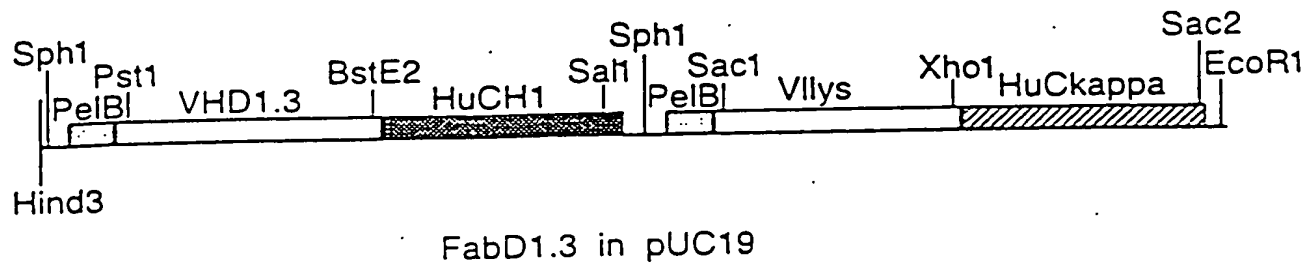


Fig.11.

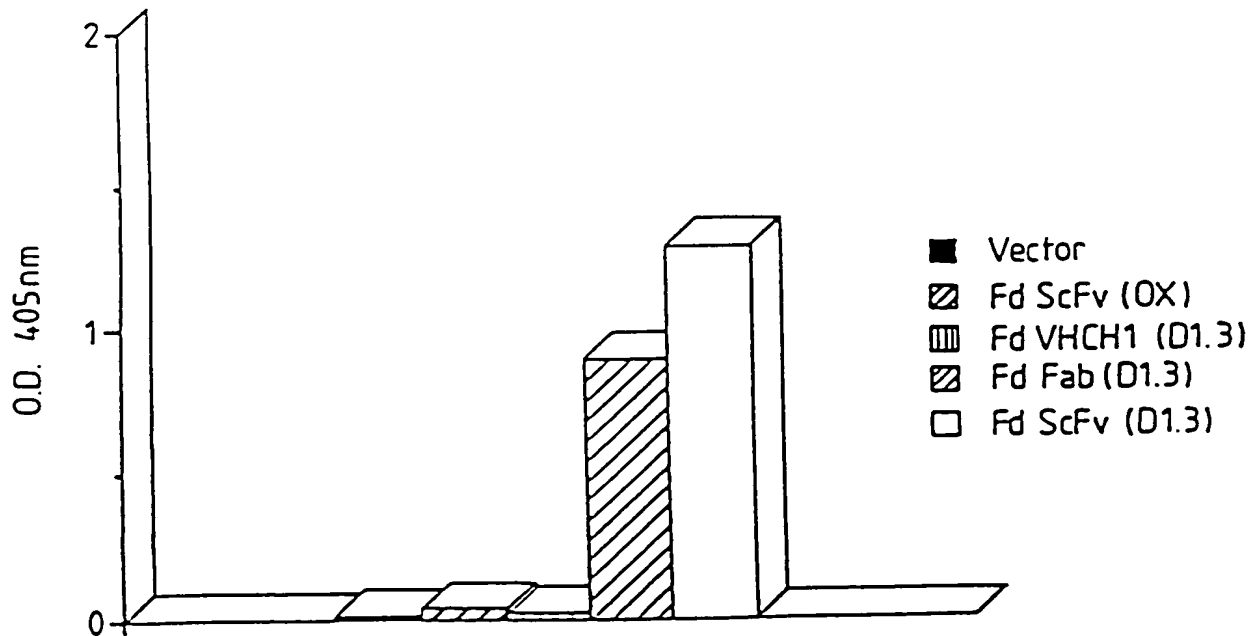


Fig.12a.

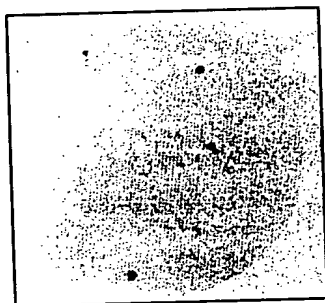


Fig.12b.

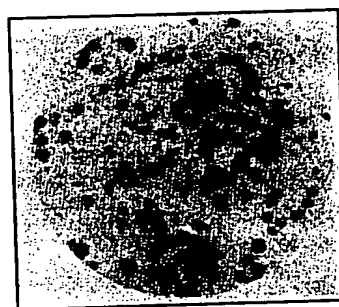


Fig.13.

Q V Q L Q E S G G G L V Q P G G
 CAG GTG CAG CTG CAG GAG TCA GGA GGA GGC TTG GTA CAG CCT GGG GGT
 PstI
 S L R L S C A T S G F T F S N Y
 TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG TTC ACC TTC AGT AAT TAC
 Y M G W V R Q P P G K A L E W L
 TAC ATG GGC TGG GTC CGC CAG CCT CCA GGA AAG GCA CTT GAG TGG TTG
 G S V R N K V N G Y T T E Y S A
 GGT TCT GTT AGA AAC AAA GTT AAT GGT TAC ACA ACA GAG TAC AGT GCA
 S V K G R F T I S R D N F Q S I
 TCT GTG AAG GGG CGG TTC ACC ATC TCC AGA GAT AAT TTC CAA AGC ATC
 L Y L Q I N T L R T E D S A T Y
 CTC TAT CTT CAA ATA AAC ACC CTG AGA ACT GAG GAC AGT GCC ACT TAT
 Y C A R G Y D Y G A W F A Y W G
 TAC TGT GCA AGA GGC TAT GAT TAC GGG GCC TGG TTT GCT TAC TGG GGC
 Q G T L V T v s s g g g g s g g g g s
 CAA GGG ACC CTG GTC ACC gtc tcc tca ggaggaggcggttcaggcgggggtggctct
 BstEII
 g g g g s d i E L T Q T P L S L P V
 ggcggtggcggtcggac atc GAG CTC ACC CAA ACT CCA CTC TCC CTG CCT GTC
 SacI
 S L G D Q A S I S C R S S Q S I
 AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT
 V H S N G N T Y L E W Y L Q K P
 GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTG CAG AAA CCA
 PstI
 G Q S P K L L I Y K V S N R F S
 GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA TTT TCT
 G V P D R F S G S G S G T D F T
 GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCG GGG ACA GAT TTC ACA
 L K I S R V E A E D L G V Y Y C
 CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC
 F Q G S H V P Y T F G G G T K L
 TTT CAA GGT TCA CAT GTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTC
 E I K R
GAG ATC AAA CGG (SEQ ID NO. 190)
 XhoI (SEQ ID NO. 191)

Fig.14.

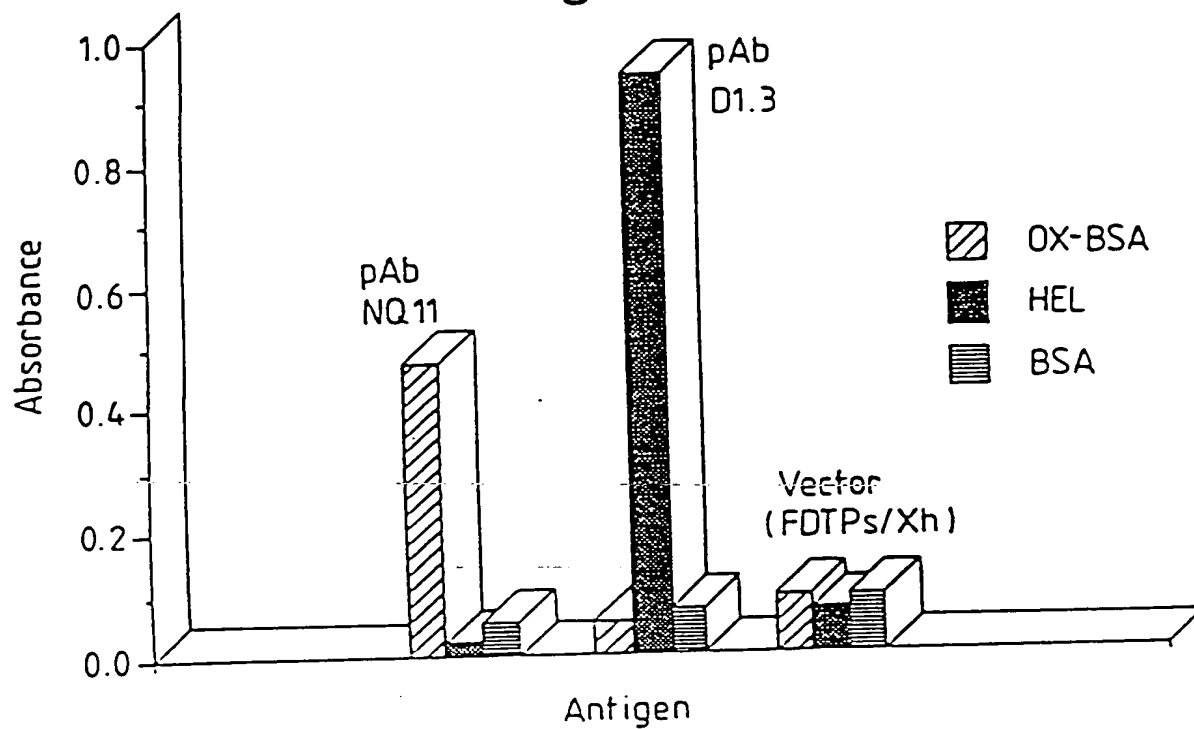


Fig.15.

5' END

TCT CAC AGT GCA CAA ACT GTT GAA CGG ACA CCA GAA ATG CCT GTT CTG (SEQ ID NO. 192)
 (SEQ ID NO. 193)
 ApaL1

3' END

K A A L G L K
 AAA GCC GCT CTG GGG CTG AAA GCG GCC GCA GAA ACT GTT GAA AGT etc.
 Not I

Fig. 16a

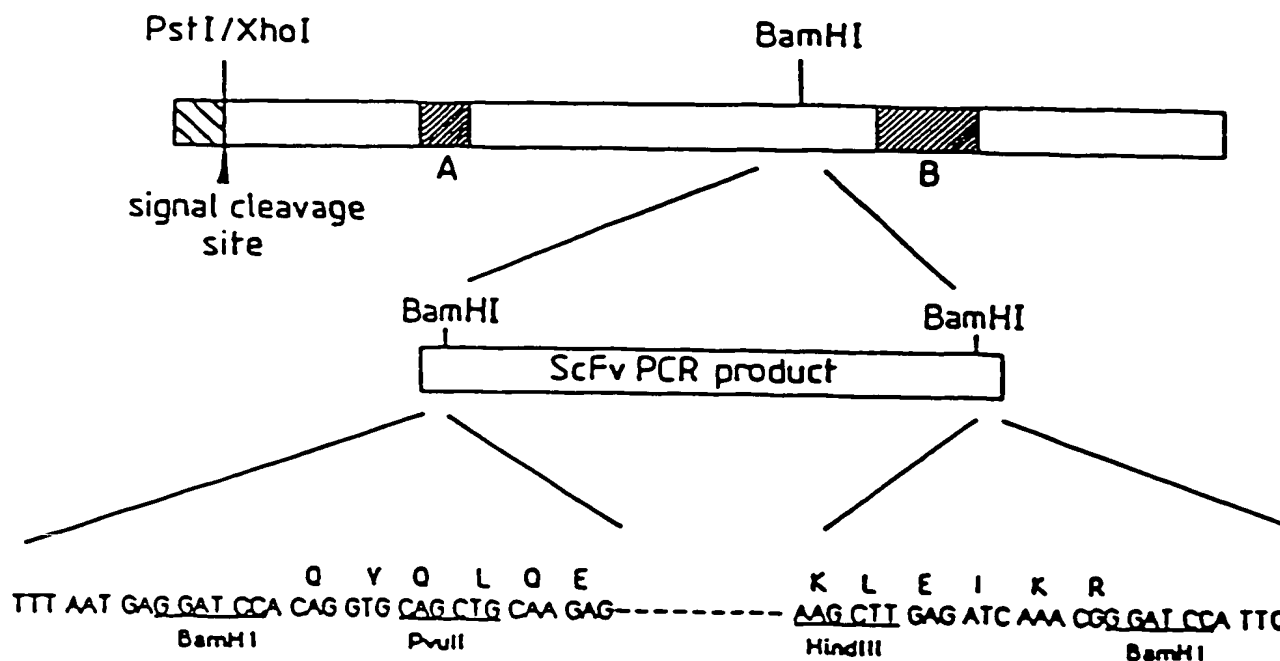
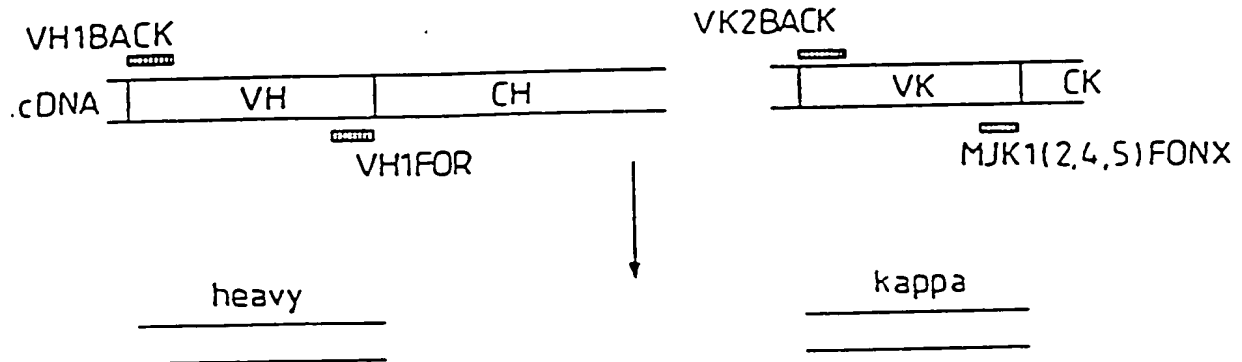


Fig. 16b

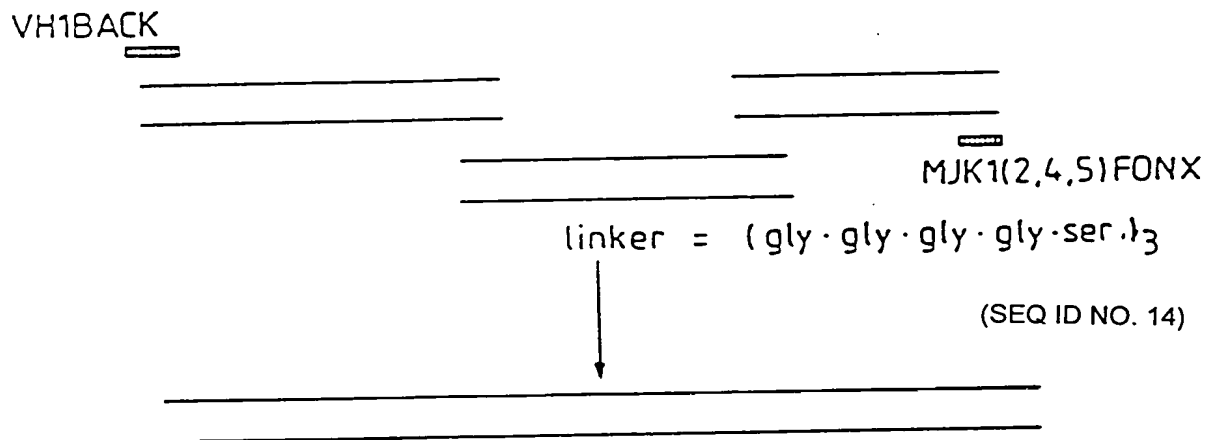
A	(1834)	5'	GAG GGT GGT GGC TCT	(SEQ ID NO. 200)
		-	- T - -	(SEQ ID NO. 201)
		-	- T - -	(SEQ ID NO. 202)
		-	- T - ACT 3'(1839)	(SEQ ID NO. 203)
B	(2284)	5'	GGC GGC GGC TCT	(SEQ ID NO. 204)
		-	GGT GGT GGT -	(SEQ ID NO. 205)
		-	GGC GGC -	(SEQ ID NO. 206)
		GAG	- GGC -	(SEQ ID NO. 207)
		-	- GGT -	(SEQ ID NO. 208)
		-	- GGC -	(SEQ ID NO. 209)
		-	- GGT -	(SEQ ID NO. 210)
		-	- GGC - 3'(2379)	(SEQ ID NO. 211)
Reverse complement of mutagenic oligo G3Bamlink				
		5'	GAG GGT GGC GGA TCC	(SEQ ID NO. 212)
			GAG GGT GGC GG 3'	(SEQ ID NO. 213)

Fig.17.

1) PRIMARY PCR



2) ASSEMBLY PCR



3) ADDING RESTRICTION SITES

VHBKAPA10

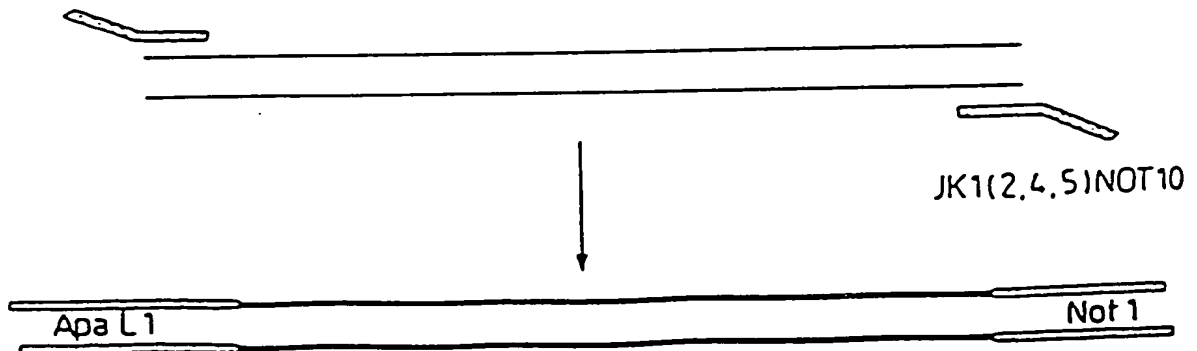


Fig.18.

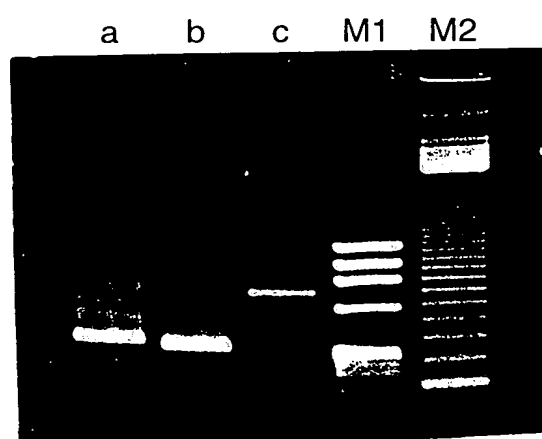


Fig.19.

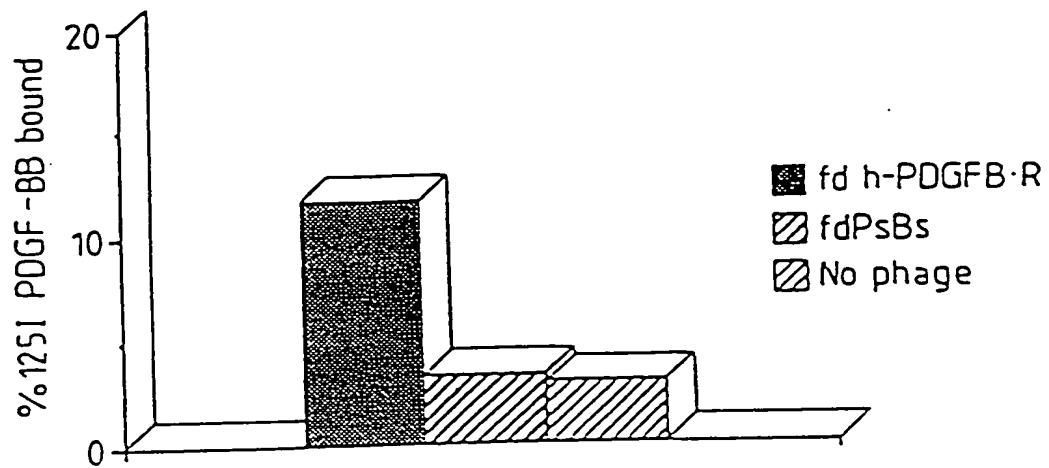


Fig.20.

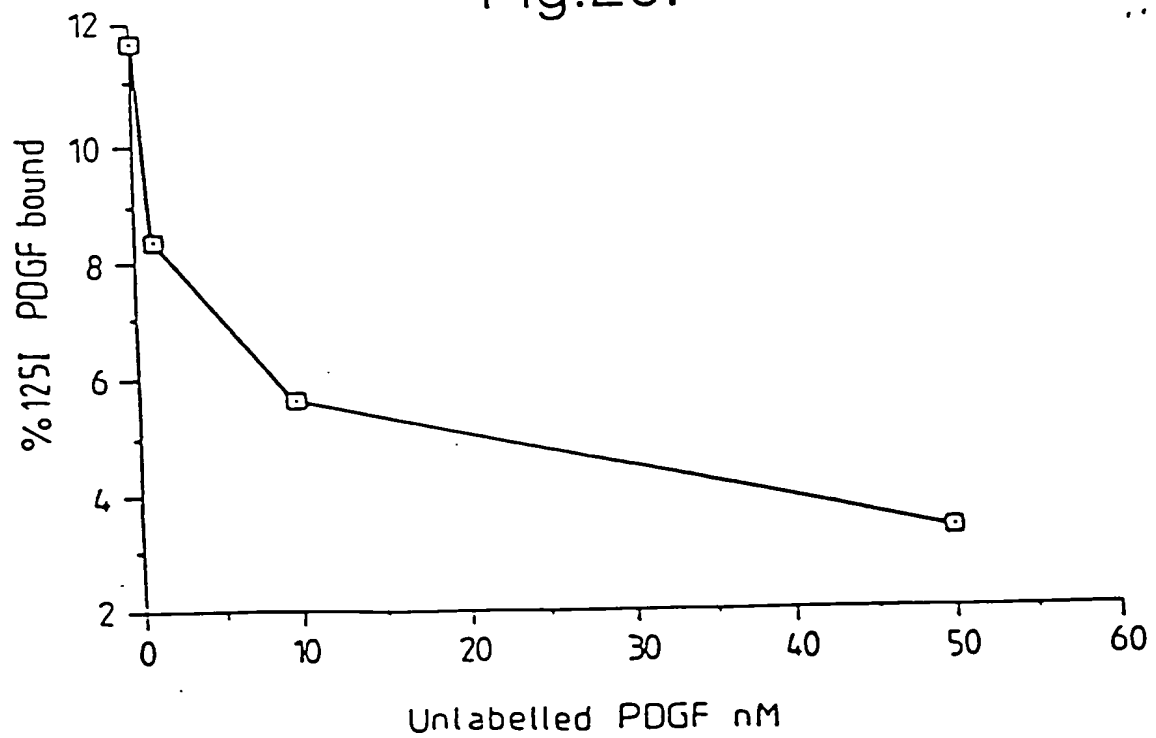


Fig.21.

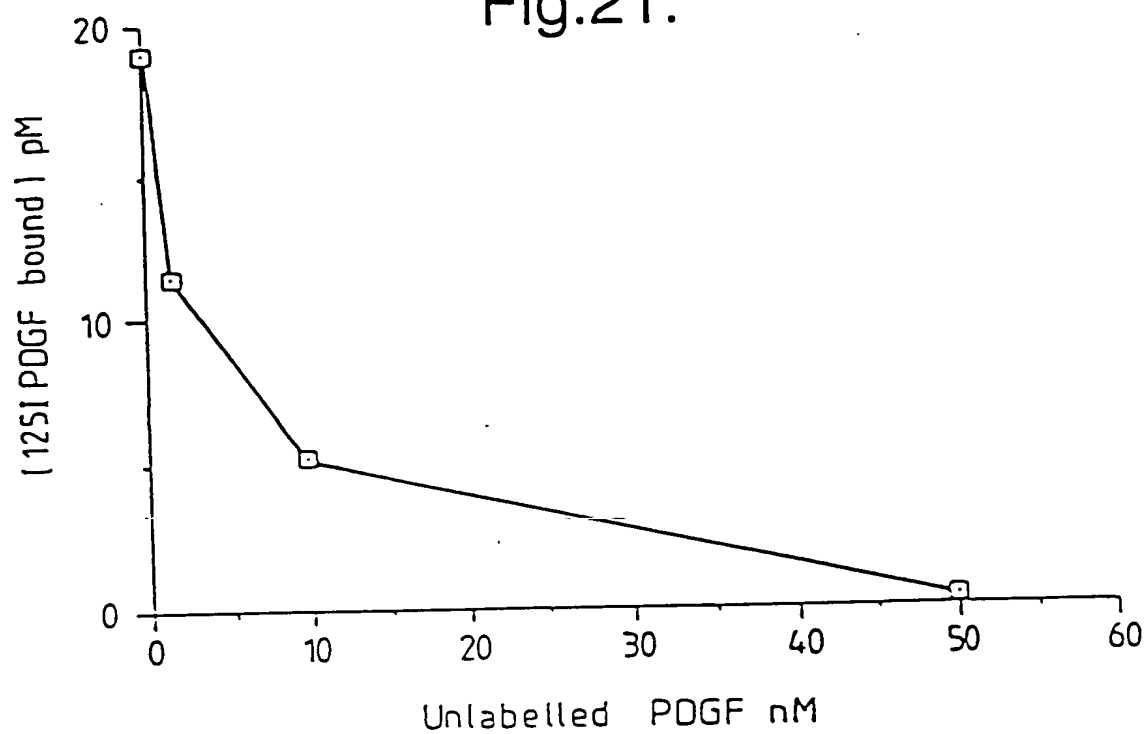


Fig.22.

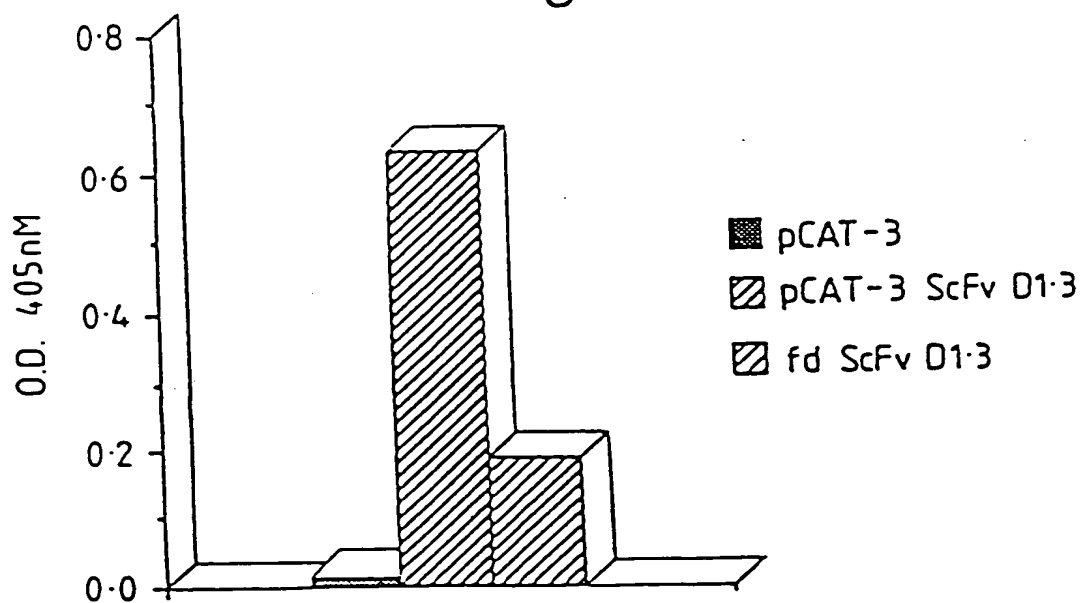


Fig. 23a

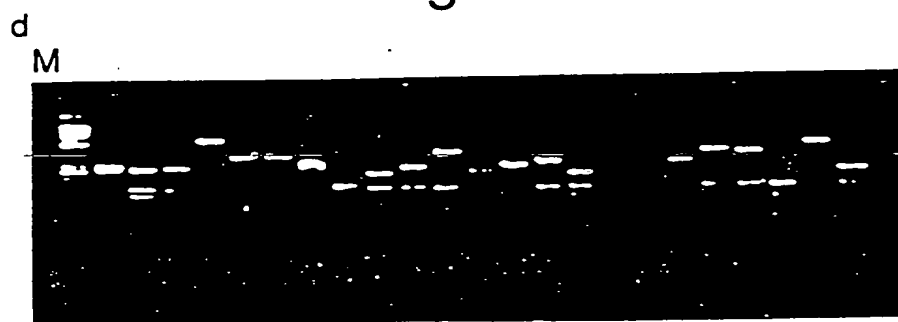


Fig. 23b

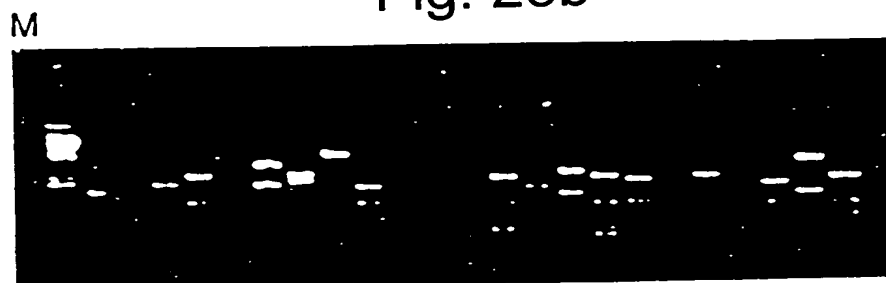


Fig. 24a

VH sequences

from combinatorial library:

	CDR1		CDR2		CDR3		
A	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSCGYTHYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	RYGAY	(SEQ ID NO. 214)
B	QVQLQQS0AELAKPGAEVXHSCKASGTTT	RDTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	NYGLY	(SEQ ID NO. 215)
C	QVQLQQSGPELVXPGA6VXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	YRSPFY	(SEQ ID NO. 216)
D	QVQLQQS0PELVXPGA6VXHSCKASGTTT	GYTHI	WVKQRPQCGLEWIG	RIHPYHODTFYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	ITTRFAY	(SEQ ID NO. 217)
E	QVQLQEGGPOLVAPQSLSITCTV80FSLT	SYTHI	WVKQRPQCGLEWIG	VIWAGSTYTHYHQAHS	RLSISKHNSK5QVFLXPRISLQTD0DDTAHYTCAR	URGDY	(SEQ ID NO. 218)
F	QVQLQQSGPELVXPGA6VXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 219)
G	QVQLQQS0AELVRPGA6VXHSCKASGTTT	RYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	ENLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 220)
H	QVQLQQSGPELVXPGA6VXHSCKASGTTT	RYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGRD	(SEQ ID NO. 221)

from hierarchical library VH-rep x Vc-d:

I	QVQLQQS0PELVXPGA6VXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	VIETNGHITHYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 222)
J	QVQLQQS0AELARPGASVXHSCKASGTTT	RYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DRGAY	(SEQ ID NO. 223)
K	QVQLQQS0AELARPGASVXHSCKASGTTT	RDTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	NYGLY	(SEQ ID NO. 224)
L	QVQLQQSGPELVXPGA6VXHSCKASGTTT	NYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 225)
M	QVQLQQS0AELARPGASVXHSCKASGTTT	NYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 226)
N	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 227)
O	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 228)
P	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 229)
Q	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 230)
R	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 231)
S	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 232)
T	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 233)
U	QVQLQQS0AELARPGASVXHSCKASGTTT	SYTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 234)
V	QVQLQQS0AELARPGASVXHSCKASGTTT	RDTHI	WVKQRPQCGLEWIG	YINPSTGYTEYHQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	DYGY	(SEQ ID NO. 235)

Fig. 24b

V_K sequences

from combinatorial library:

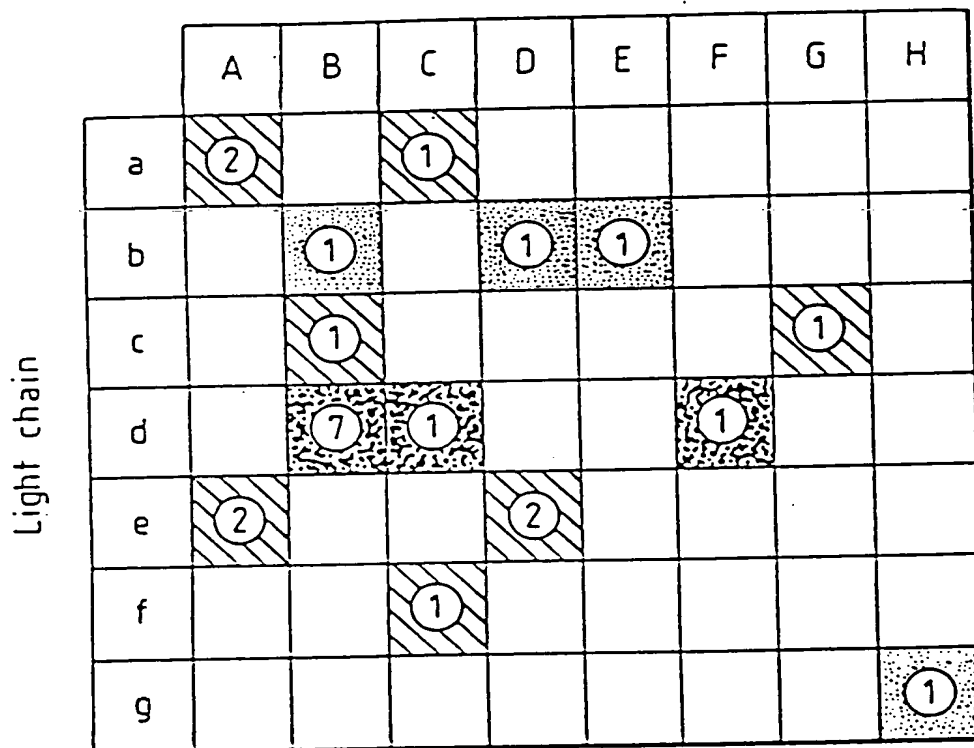
	CDR1	CDR2	CDR3		
a	RAEQEISCTLS	WLOQKPGCSIKRLIY	LOYASYPT	FCAGTKLEIKRA	x3
b	RASSSV66SYLH	WYQKSGASPKRMII	QYSGYPLT	FCAGTKLEIKRA	x3
c	SASSS16SNTLH	WYQKPGFSPKLLIY	QCGSSIPLT	FCAGTKLEIKRA	x3
d	SASSS16SNTLH	WYQKPGFSPKLLIS	QCGSTIPPT	FCAGTKLEIKRA	x9
e	SASSSVNTDII	WYQKPGCTSPKLMII	QQRSSYPPT	FCAGTKLEIKRA	x4
f	SASSSV5YIN	WYQKSGTSPKRMII	QQFSRIPLT	FCAGTKLEIKRA	x1
g	SASSSINTDII	WYQKPGASPKRMII	IQNRNYPPT	FCAGTKLEIKRA	x1

from hierarchical library VII-B x V_K-rep:

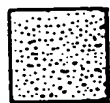
h	SASSSV5TDII	DTSKLA9	QW6SRIPLT	FCAGTKLEIKRA	x4	IV/VI	V _K ox1	(SEQ ID NO. 243)
i	SASSSV6TIIH	STSHLA9	QWTHSIPLT	FCAGTKLEIKRA	x3	V	ox-1ike	(SEQ ID NO. 244)
j	SASSS16SNTLH	RTSHLA9	QCGSSIPLT	FCAGTKLEIKRA	x3	V	ox-1ike	(SEQ ID NO. 245)
k	SATS61SSNTLH	RTSHLA9	QCGSIPPT	FCAGTKLEIKRA	x3	V	ox-1ike	(SEQ ID NO. 246)
l	SASSS16SNTLH	RTSHLA9	QCGSIPPT	FCAGTKLEIKRA	x3	V	ox-1ike	(SEQ ID NO. 247)
m	SASSS16SNTLH	RTSHLA9	QCGSIPPT	FCAGTKLEIKRA	x3	V	ox-1ike	(SEQ ID NO. 248)
n	SASSS16SNTLH	RTSHLA9	QCGSIPPT	FCAGTKLEIKRA	x3	V	ox-1ike	(SEQ ID NO. 249)
o	SASSS16SNTLH	RTSHLA9	QCGSIPPT	FCAGTKLEIKRA	x3	V	ox-1ike	(SEQ ID NO. 250)
p	SASSSV5TDII	DTSKLA9	QW6SRIPLT	FCAGTKLEIKRA	x3	IV/VI	V _K ox1	(SEQ ID NO. 251)
q	SASSSV5TDII	DTSKLA9	QWTHSIPLT	FCAGTKLEIKRA	x3	IV/VI	V _K ox1	(SEQ ID NO. 252)
r	SASSSV6TIIH	DTSKLA9	QWTHSIPLT	FCAGTKLEIKRA	x3	IV/VI	V _K ox1	(SEQ ID NO. 253)
s	RASSSV58YIN	RTSHLA9	QYSGYPLT	FCAGTKLEIKRA	x3	IV/VI	ox-1ike	(SEQ ID NO. 254)
t	RASSSV96SYLH	RTSHLA9	QQRSSYPPT	FCAGTKLEIKRA	x3	IV/VI	ox-1ike	(SEQ ID NO. 255)
u	RASSSV56SYLH	RTSHLA9	QYSGYPLT	FCAGTKLEIKRA	x3	IV/VI	ox-1ike	(SEQ ID NO. 256)
v	RASSSV56SYLH	RTSHLA9	QYSGYPLT	FCAGTKLEIKRA	x3	IV/VI	ox-1ike	(SEQ ID NO. 257)
w	SASSS16SNTLH	RTSHLA9	QCGSIPPT	FCAGTKLEIKRA	x3	IV/VI	ox-1ike	(SEQ ID NO. 258)

Fig.25.

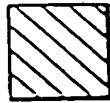
HEAVY CHAIN



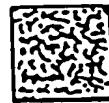
OD_{405nm} in ELISA



0.2-0.9



0.9-2.0



>2.0

Fig.26(a).

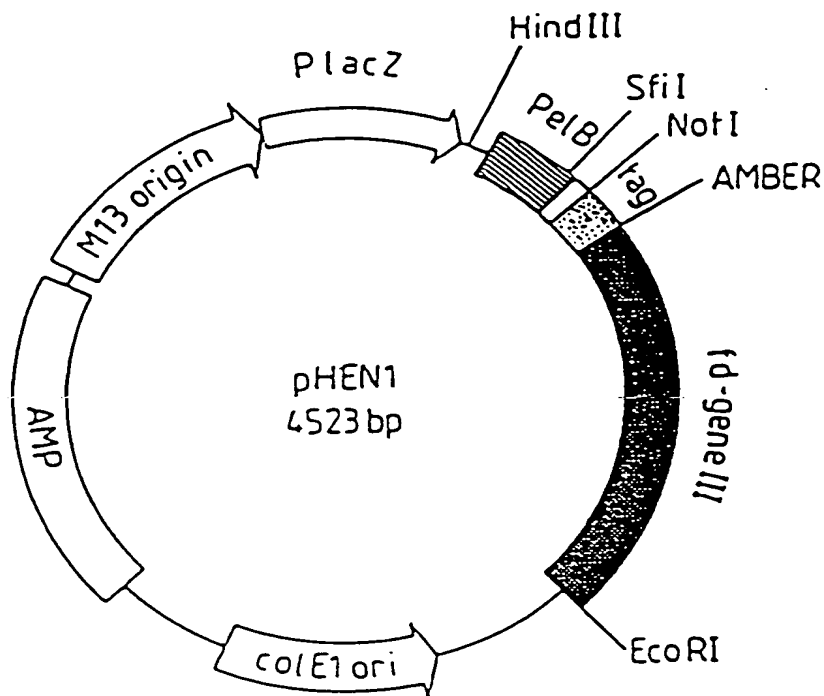


Fig.26(b).

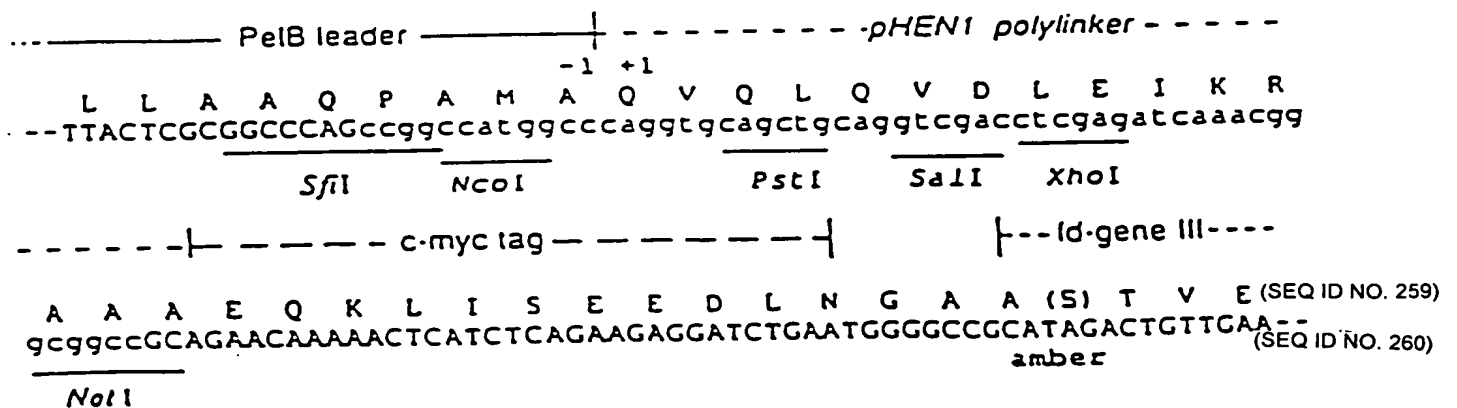


Fig.27.

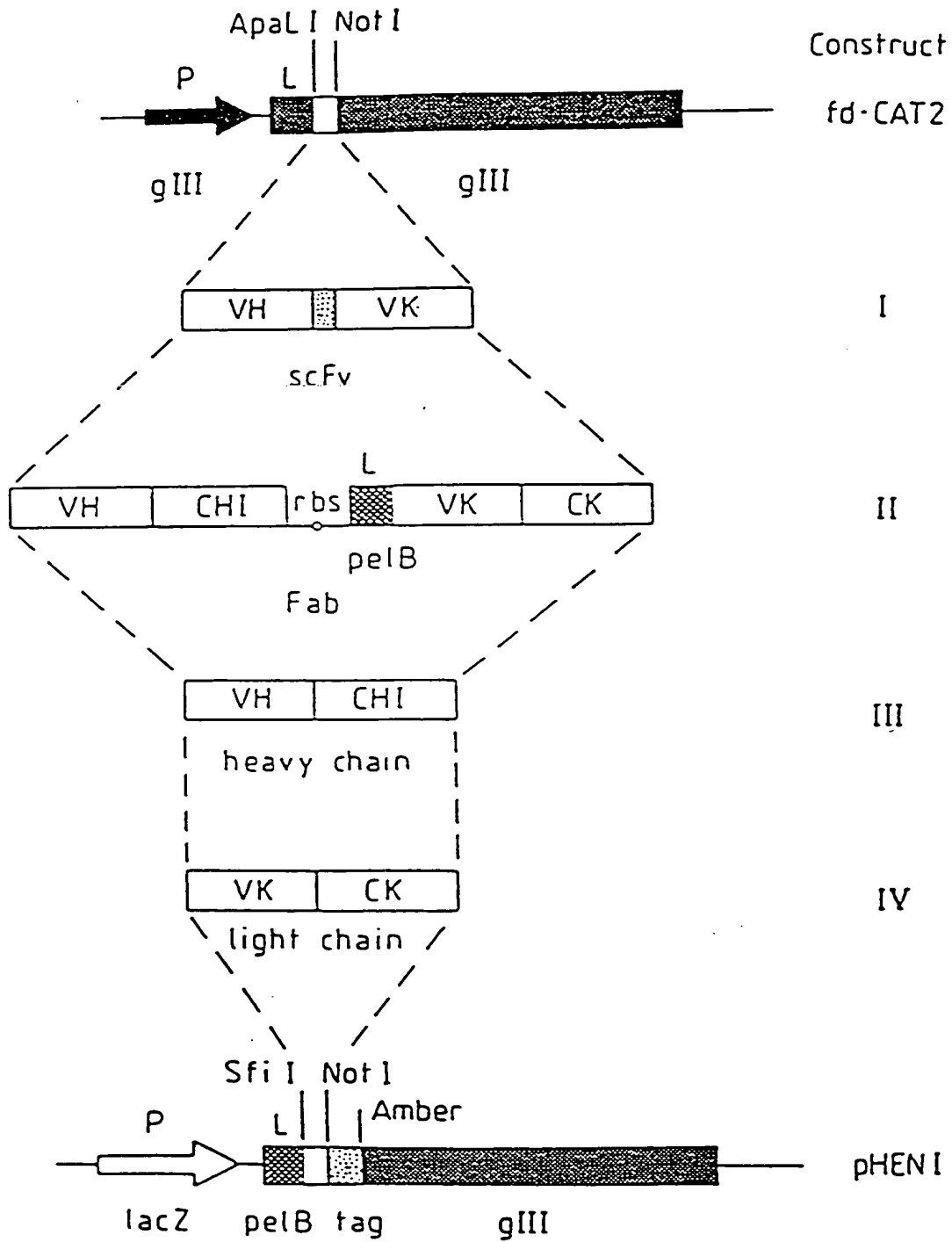


Fig.28.

Fab

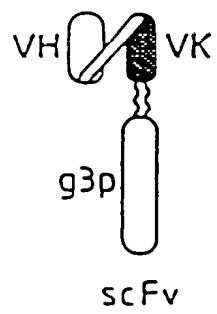
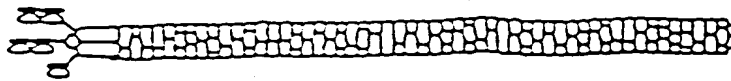
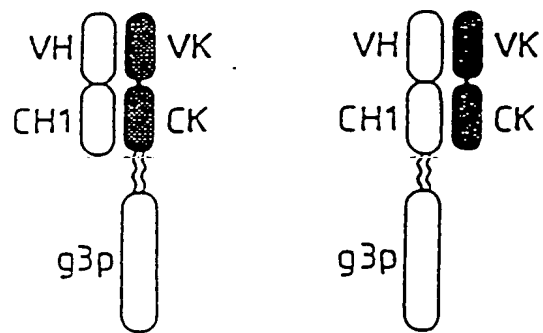


Fig.29.

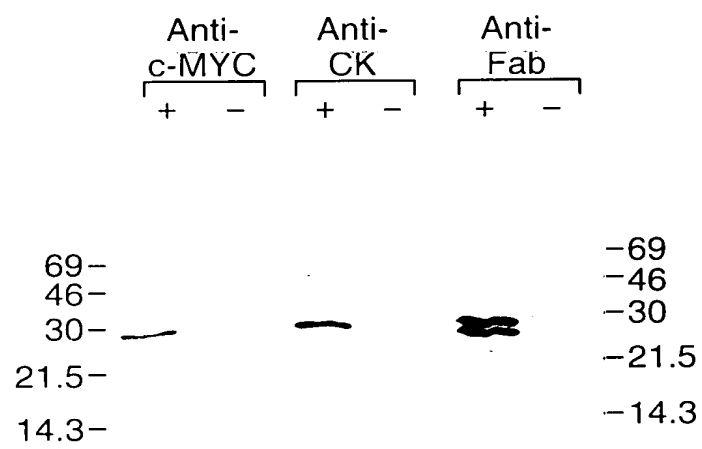


Fig.30.

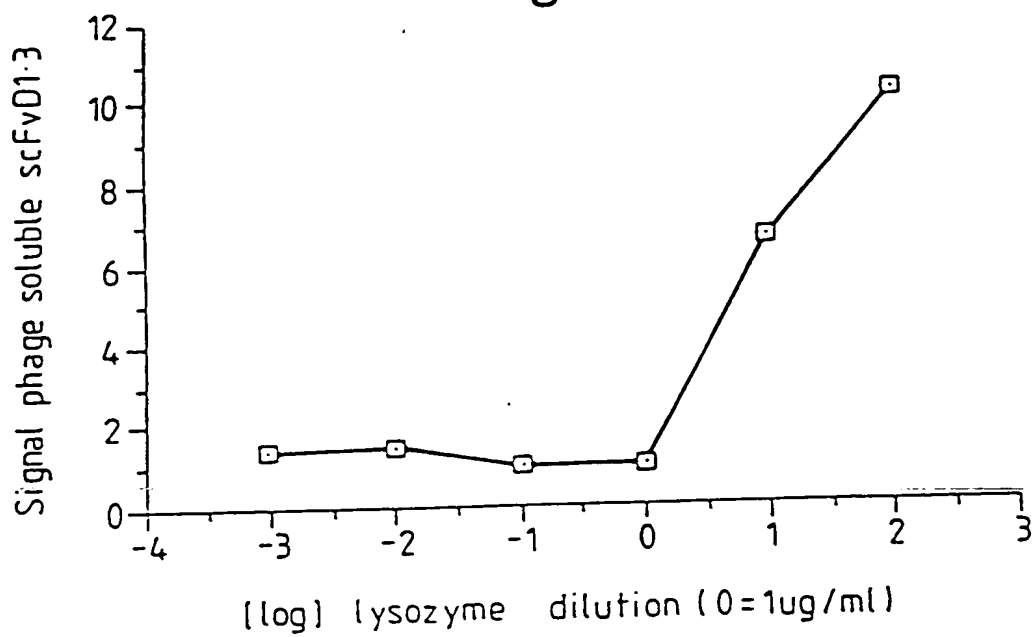


Fig.31.

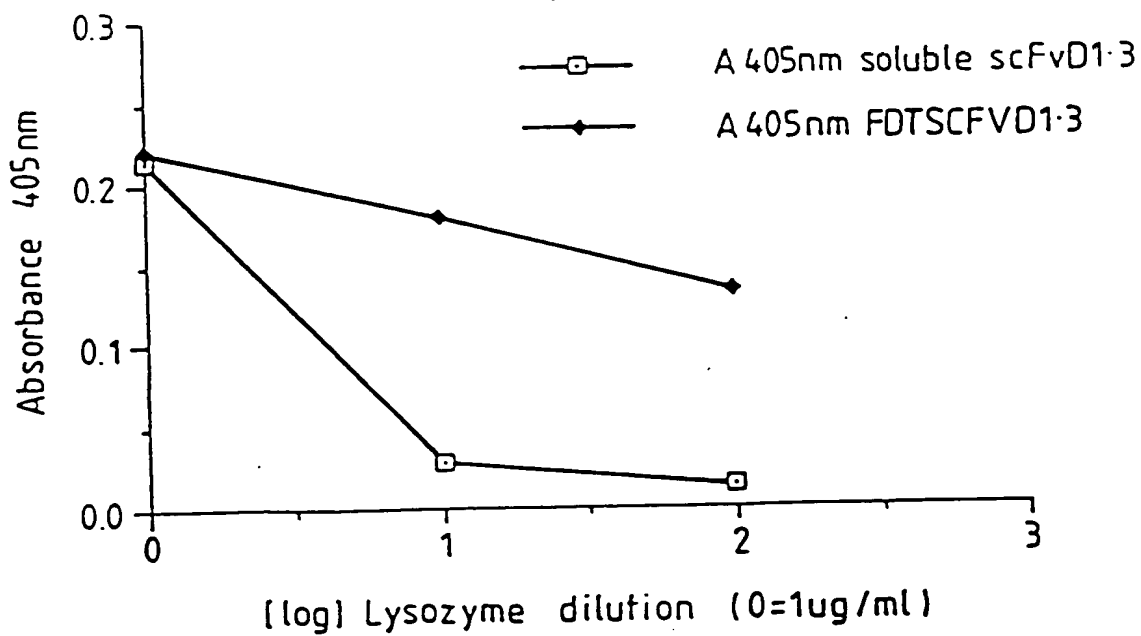


Fig.32.

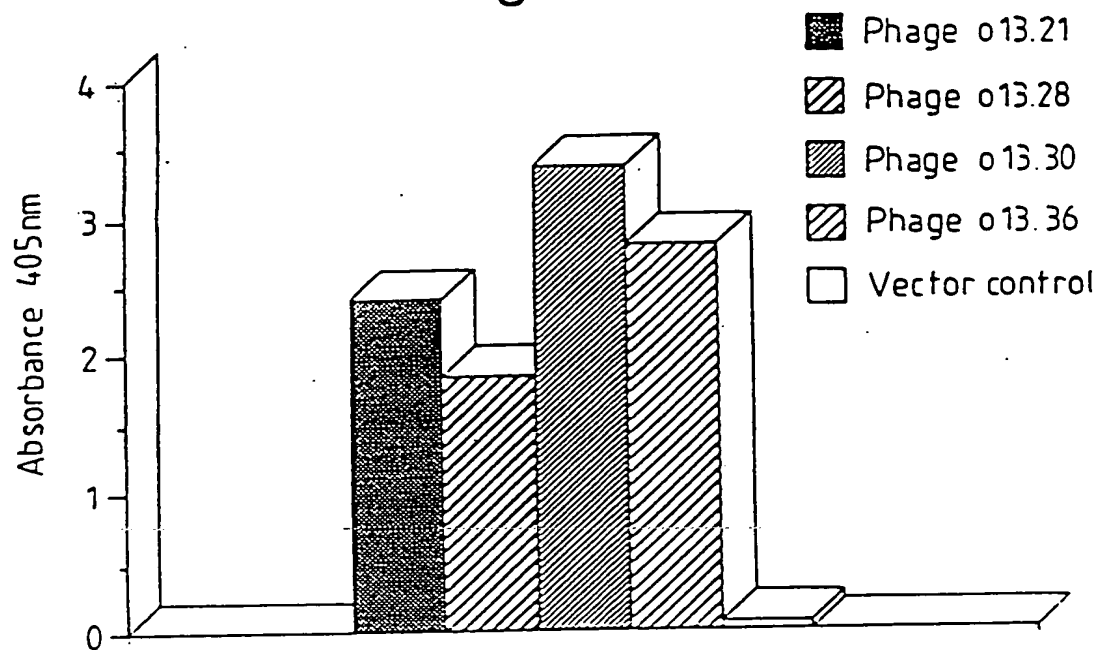


Fig.33.

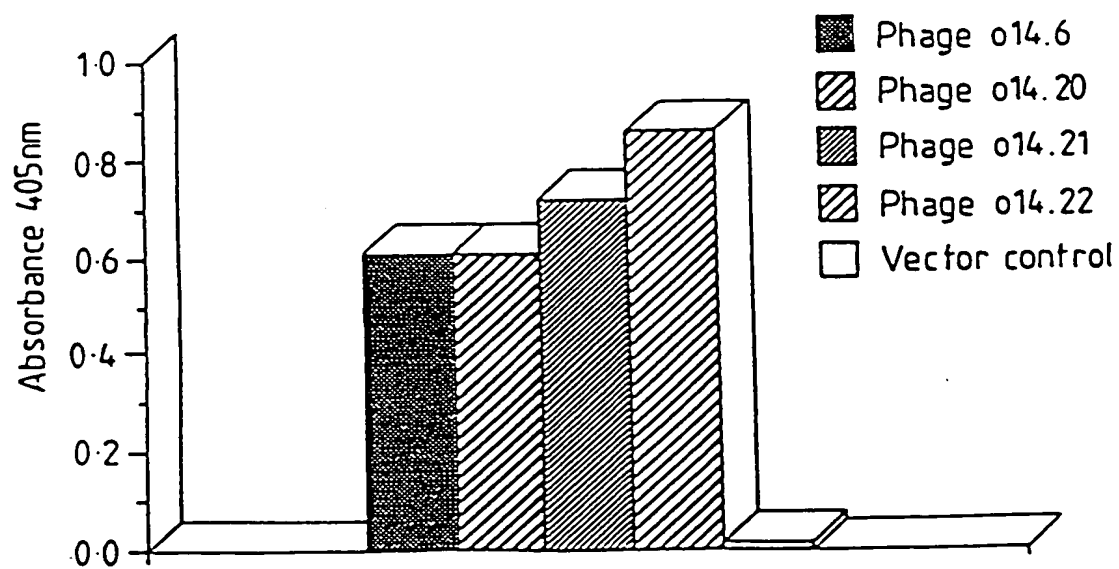


Fig.34.



Fig.35A.

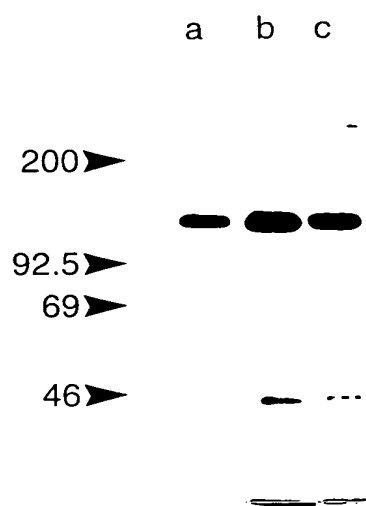


Fig.35B.

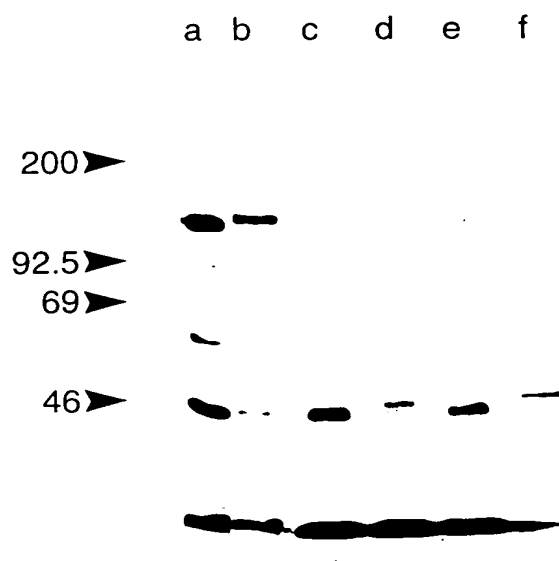


Fig.36.

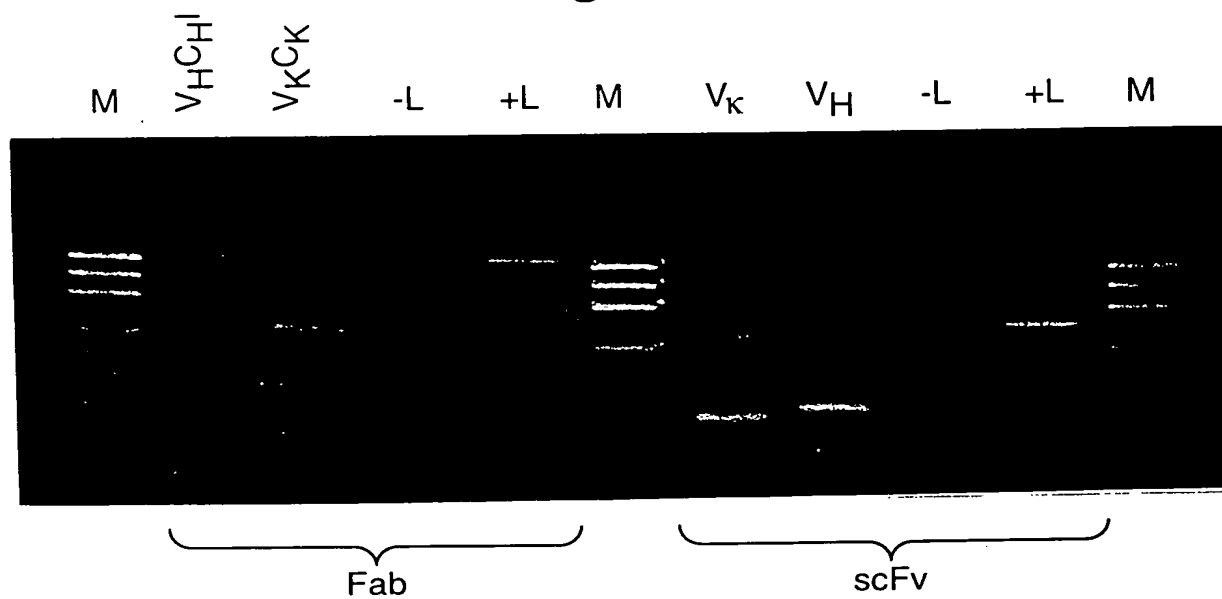


Fig.37.

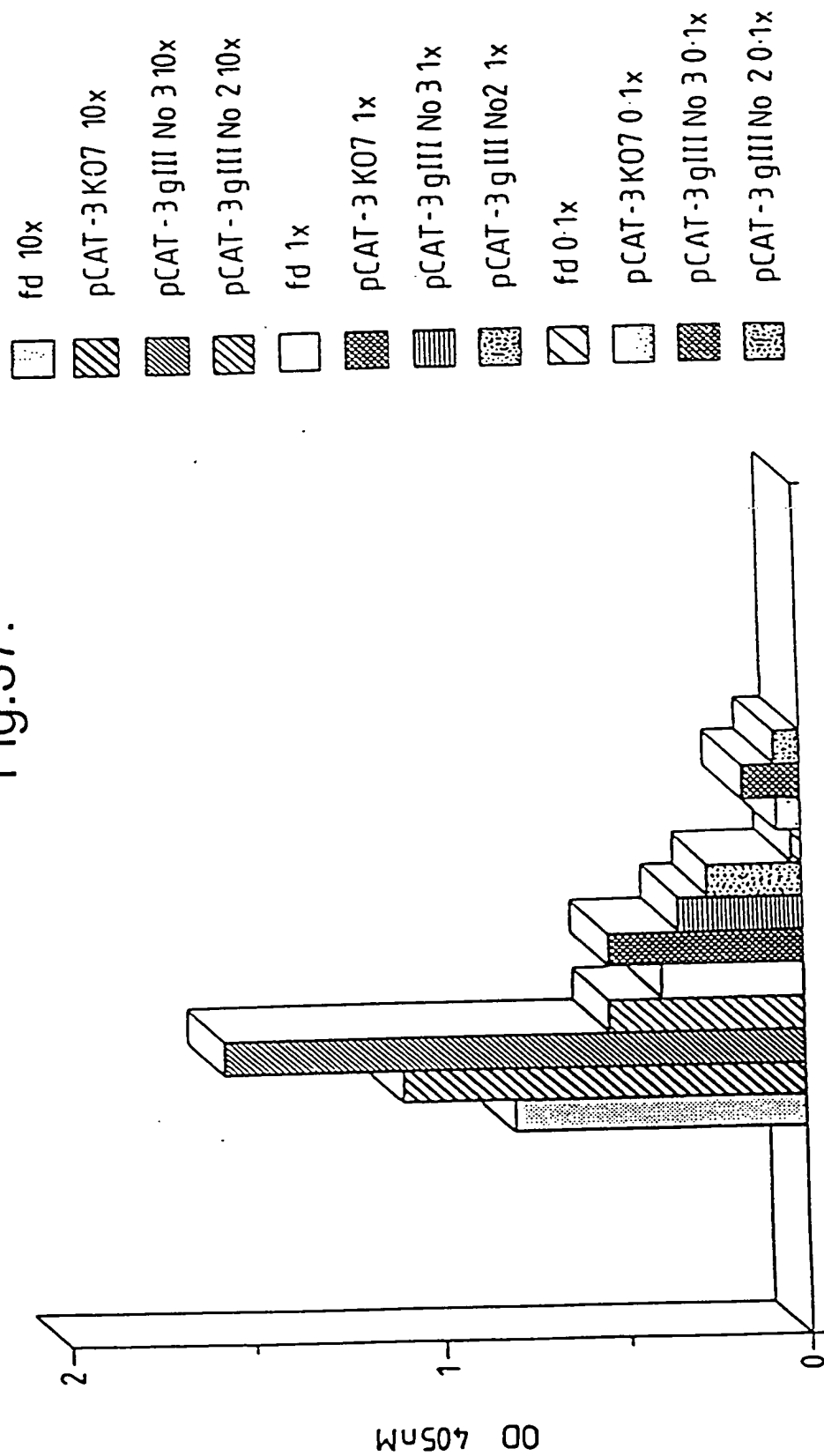


Fig.38A.

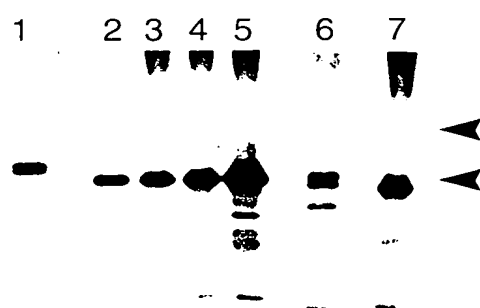


Fig.38B.

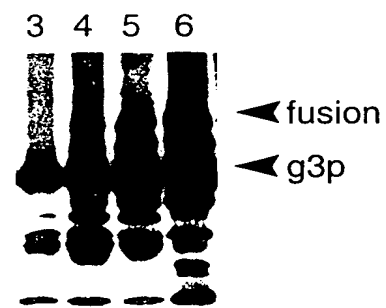


Fig.39.

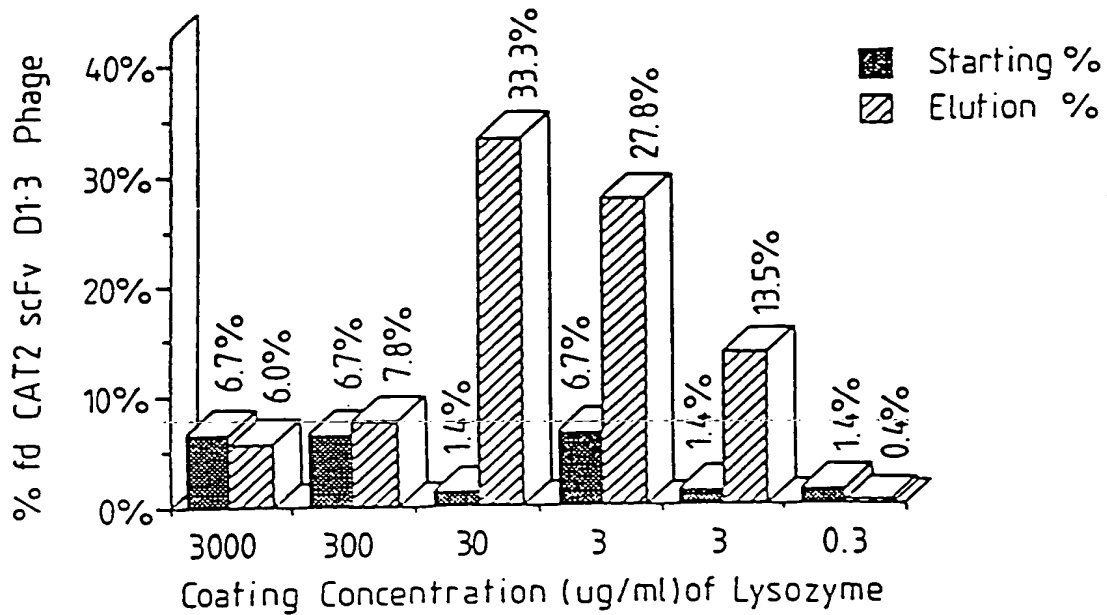


Fig.40.

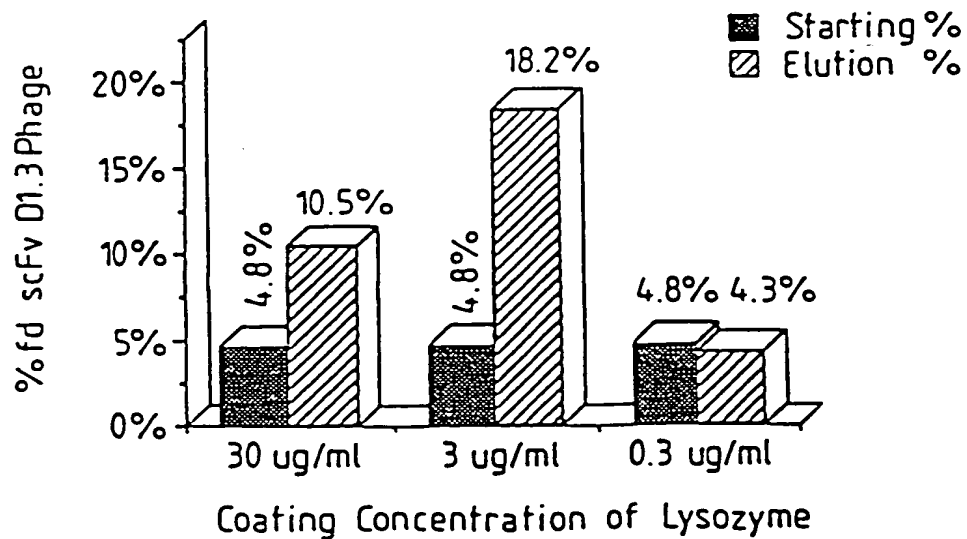


Fig.41.

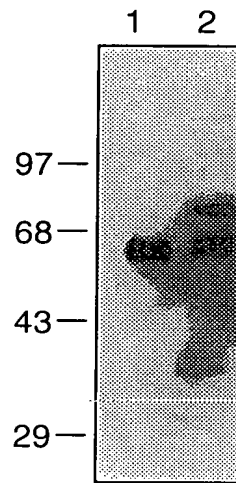


Fig.42.



Fig.43.

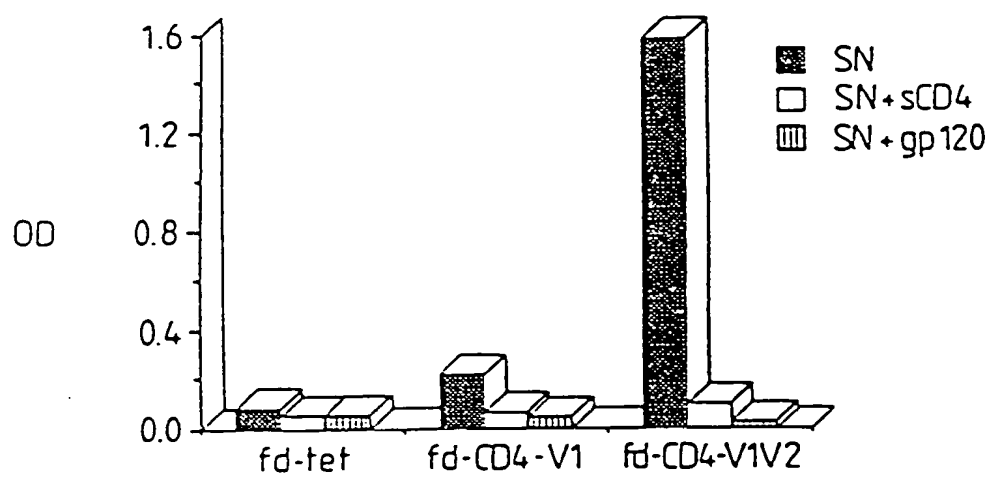


Fig. 44a

10 20 30 40 50 60 70 80 90
 TTCTATTCTCACNGTGCNCAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGNAAGCCTGGGGCTTCAGTGAGCTGTCTCTGCAAGGCT
 AAGATAAGAGTGTACGTTGTCAGGTCGACGTCGTAGACCCCGACTCGAACACTTCGGNACCCCGAAGTCACCTTCGACAGGACGTTCCGA
 PheTyrSerHisSerAlaGlnValGlnLeuGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysLeuSerCysLysAla
 100 110 120 130 140 150 160 170 180
 TCTGGCTACACCTTCACCACTACTGGATGCACCTGGGTGANGCAGAGGCCCTGGACGAGGCCCTTGAGTGGATTGGNAGGATTGATCCTAAT
 AGACCGATGTGGNAGTGGTCGATGACCTACGTGACCCACTTCGTCTCCGGACCTGCTCCGGNACTCACCTAACCTTCTCCTAACCTAGGATTA
 SerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgProGlyArgGlyLeuGluTrpIleGlyArgIleAspProAsn
 190 200 210 220 230 240 250 260 270
 AGTGGTGGTACTAAGTACAAATGAGNAGTTCAAGAGCMAAGGCCACACTGACTGTAGACAAACCCCTCCAGCACAGCCTACATGCAGCTCAGC
 TCACCAACCATGATTCTTACTCTTCAAGTTCTCGTTCCGGTGTGACTGACATCTGTTTGGAGGTCGTGTCGGNTGTACGTCCGAGTCG
 SerGlyGlyThrLysTyrAsnGluLysPheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAlaTyrMetGlnLeuSer
 280 290 300 310 320 330 340 350 360
 AGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGNTACGACTACGGTAGTAGCTACTACTTTGACTACTGGGGCCCAAGGGACC
 TCGGACTGTAGACTCCTGAGACGCCAGATAATAACACCGTTCTATGCTGATGCCATCATCGATGATGAACTGATGACCCCGGTTCCCTGG
 SerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrAspTyrGlySerSerTyrTyrPheAspTyrTrpGlyGlnGlyThr
 370 380 390 400 410 420 430 440 450
 ACGGTACCCGTCTCCTCNGGTGGAGGCGGTTTCAGGGCGGAGGTGGCTCTGGCGGTGGCGGATCCAGGCTGTTGGGACACAGGMAATCTGCA
 TGCCAGTGGCAGAGGATCCACCTCCGCCCAAGTCCGCCCTCCACCGAGACCGCCACCGCTAGGGTCCGACAAACCCCTGTCTCTTAGACGT
 ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlnAlaValGlyThrGlnGluSerAla
 460 470 480 490 500 510 520 530 540
 CTCACACATCACCTGGTGAACAGATCACACTACTTGTGCTCAAGTACTGGGGCTGTTACAACTAGTAACCTATGCCAACTGGGTCCAA
 GAGTGGTGTAGTGACCACTTTGTCAAGTGTGAGTGAACAGCGAGTTCAATGACCCCGACAAATGTTGATCATTTGATACCGTTGACCCAGGTT
 LeuThrThrSerProGlyGluThrValThrLeuThrCysArgSerSerThrGlyAlaValThrThrSerAsnTyrAlaAsnTrpValGln
 550 560 570 580 590 600 610 620 630
 GAAACACAGATCATTTATTCACTGGTCTAATAGGTGGTACCAACACCGAGCTCCAGGTGTTCTCGCCAGATTCTCAGGCTCCCTGATT
 CTTTGTGGTCTAGTAAATAAGTGACCAAGATTATCCACCATGTTGTTGGTCTCGAGGTCCACACAGGACGGTCTAAGAGTCCGAGGACCTAA
 GluLysProAspHisLeuPheThrGlyLeuIleGlyGlyThrAsnAsnArgAlaProGlyValProAlaArgPheSerGlySerLeuIle

Fig. 44b

640	650	660	670	680	690	700	C	G	710	720
GGAGAC	AGGCTGCC	CTCACC	ATCAC	AGGGGC	CACAG	ACTGAG	GATGAG	GCAT	TATAT	TCTCT
CCTCTG	TTCCGAC	GGGAGT	GGTAGT	GTCCCC	GTGCTG	ACTCCT	ACTCCT	ACTCCT	ACTCCT	ACTCCT
GlyAsp	LysAla	AlaLeu	ThrIle	ThrGly	AlaGln	ThrGlu	AspGlu	AlaIle	TyrPhe	CysAla
730	740	750	760	770						
TTCC	GTGGAG	GAAC	CAAACT	GTCTCT	CGAGAT	CAAA	CGGGCG	CGCGC		
AA	CCCTCT	GTGGAG	CTGACT	GTCTCT	CGAGAT	CAAA	CGGGCG	CGCGC		
AA	CCCTCT	GTGGAG	CTGACT	GTCTCT	CGAGAT	CAAA	CGGGCG	CGCGC		
PheGly	GlyGly	ThrLys	LeuThr	ValLeu	GluIle	LysArg	AlaAla			

(SEQ ID NO. 261)

(SEQ ID NO. 262)

Fig.45.

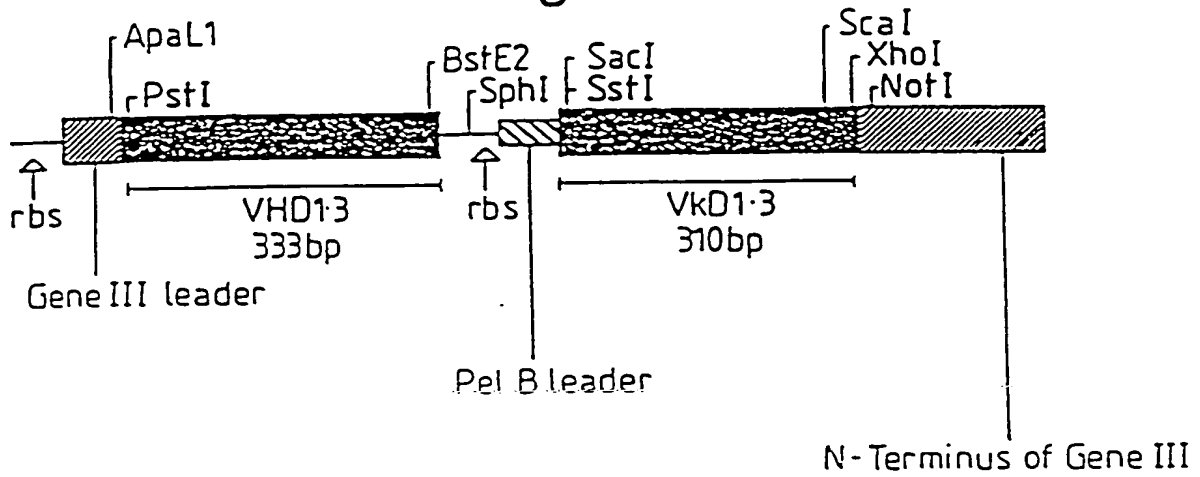


Fig.46.

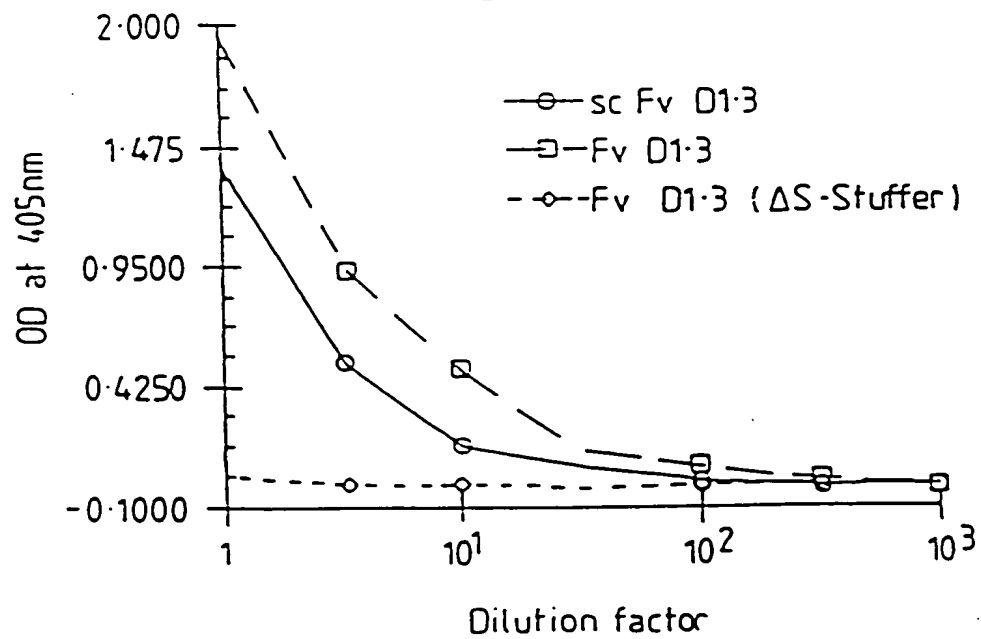


Fig.47.

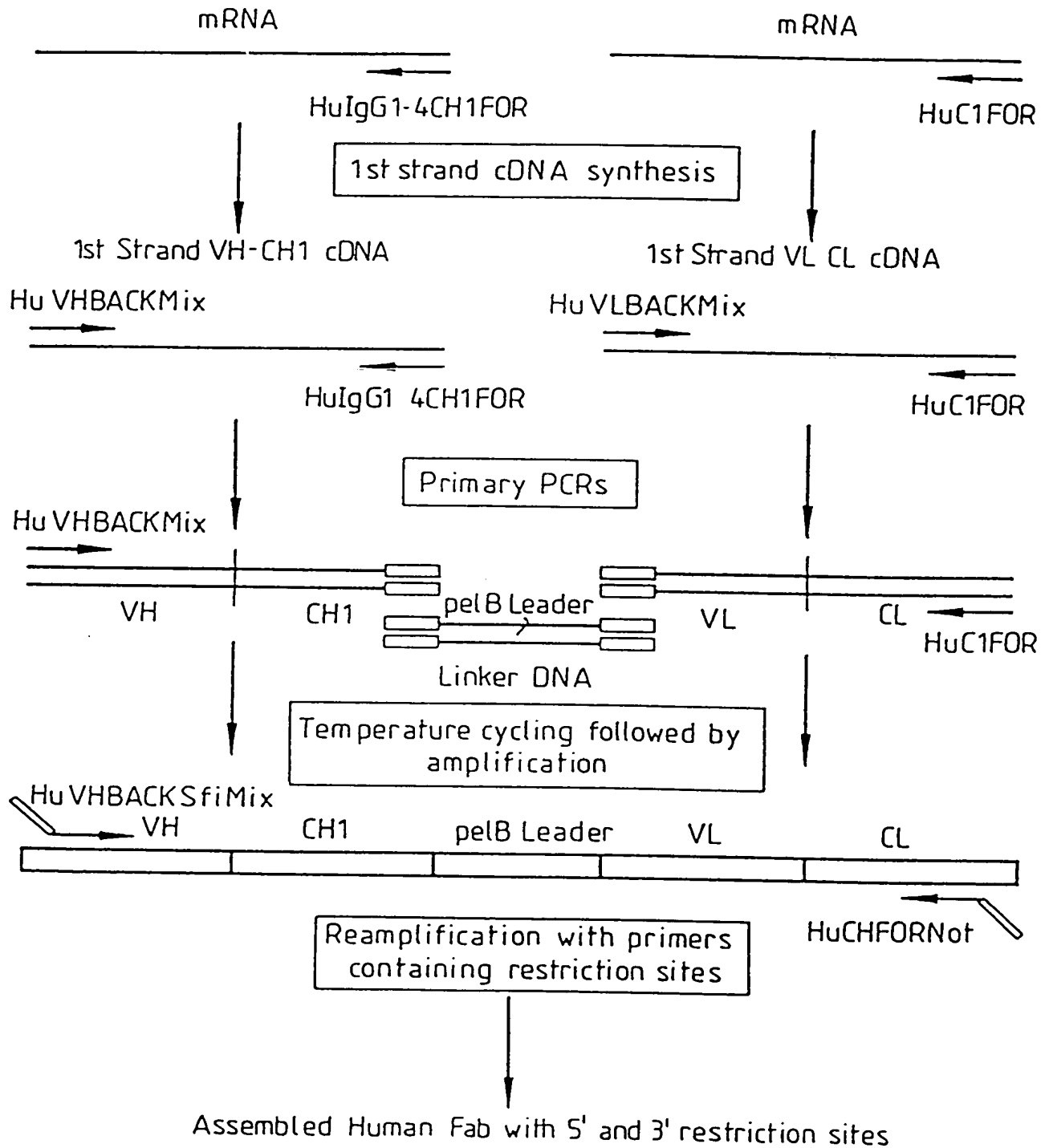


Fig. 48a

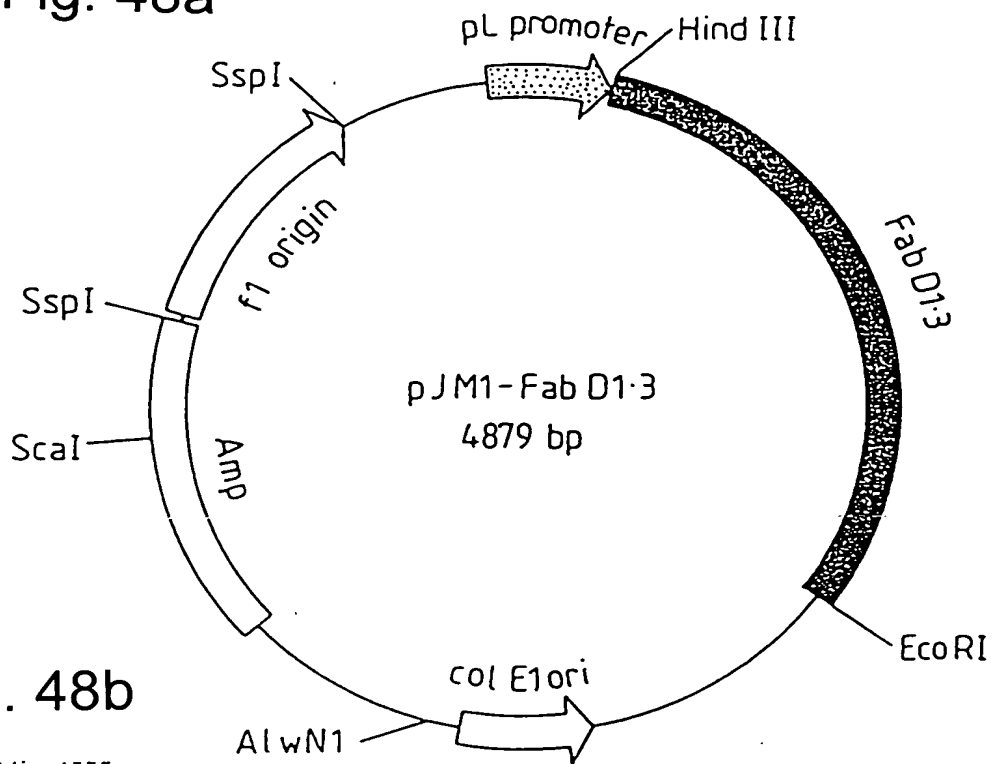


Fig. 48b

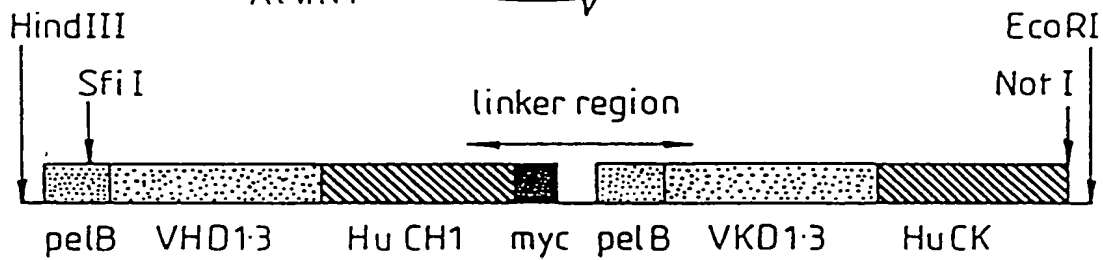


Fig. 48c

Sequence of linker region

← 3' Human CH1 and hinge →
K P S N T K V D K K V E P K S S T K T H T
AACCCAGCAACACCAAGGTCGACAAGAAAGTTGAGCCCAAATCTTCAACTAAGACGCACACA

→ myc peptide tag ←
S G G E Q K L I S E E D L N * *
TCAGGAGGTGAACAGAAGCTCATCTCAGAAGAGGATCTGAATTAATAAGGGAGCTTGCATGCA

← pelB leader →
M K Y L L P T A A A G L
AATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGT

→ 5' Vk →
L L P A A Q P A M A D I E L T Q S P
TATTAACTGCTGCCCCAACCAGOGATGGCCGACATOGAGTTCACCCAGTCTCC

Fig.49.

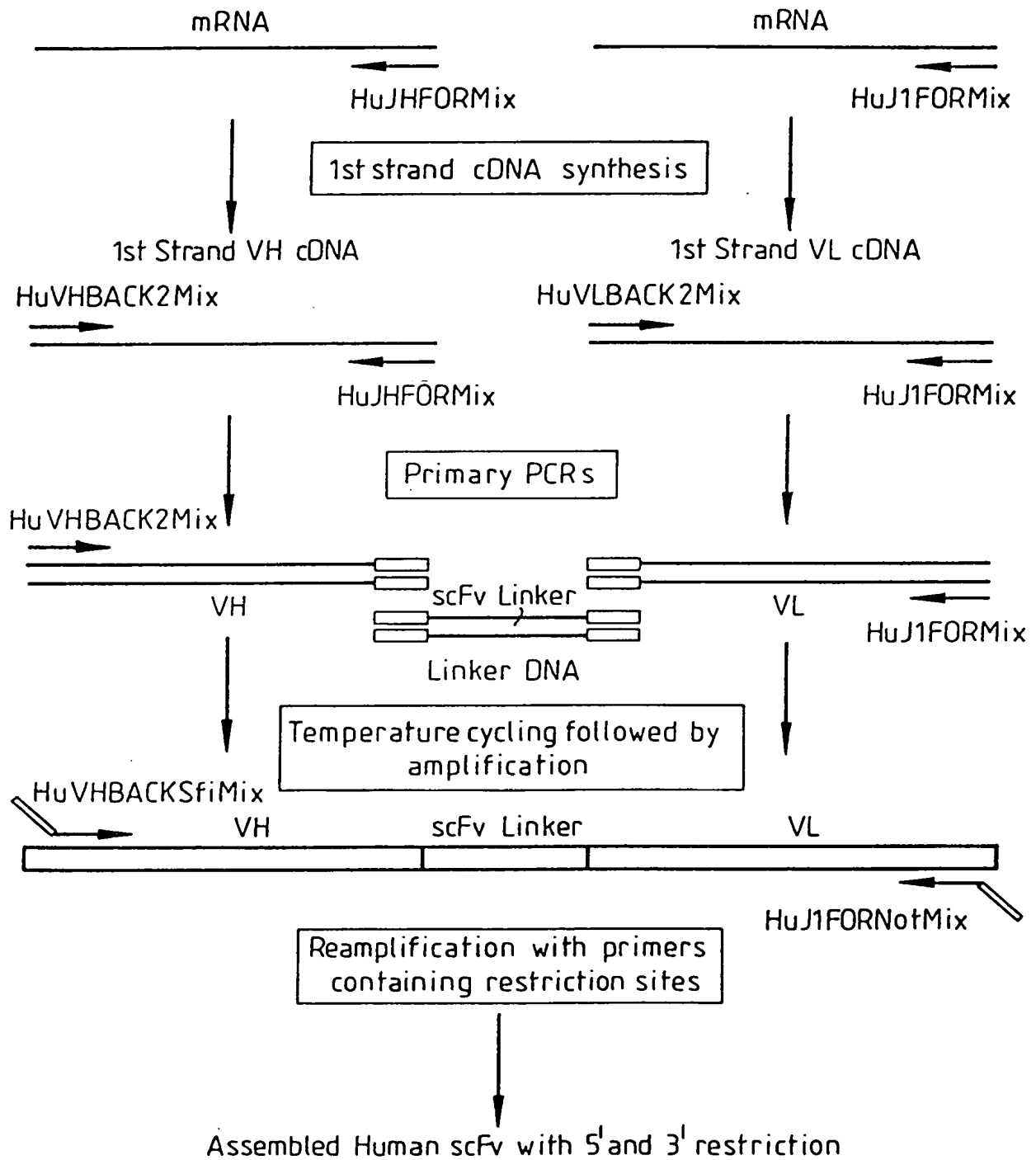


Fig. 50a

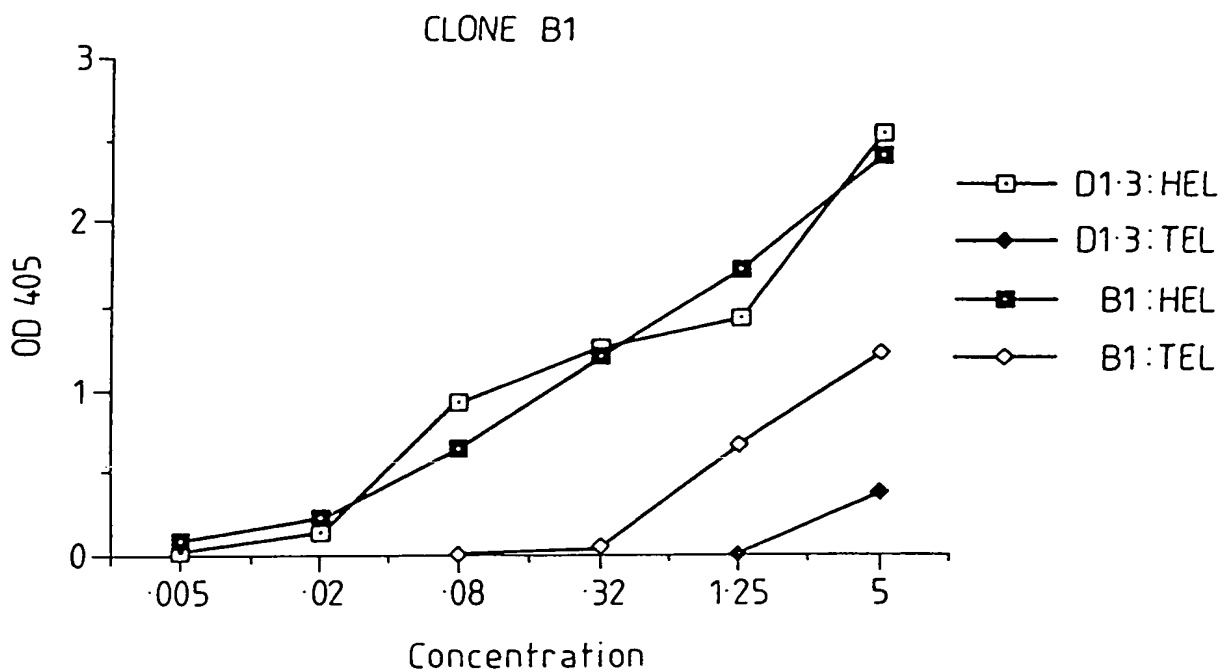


Fig. 50b

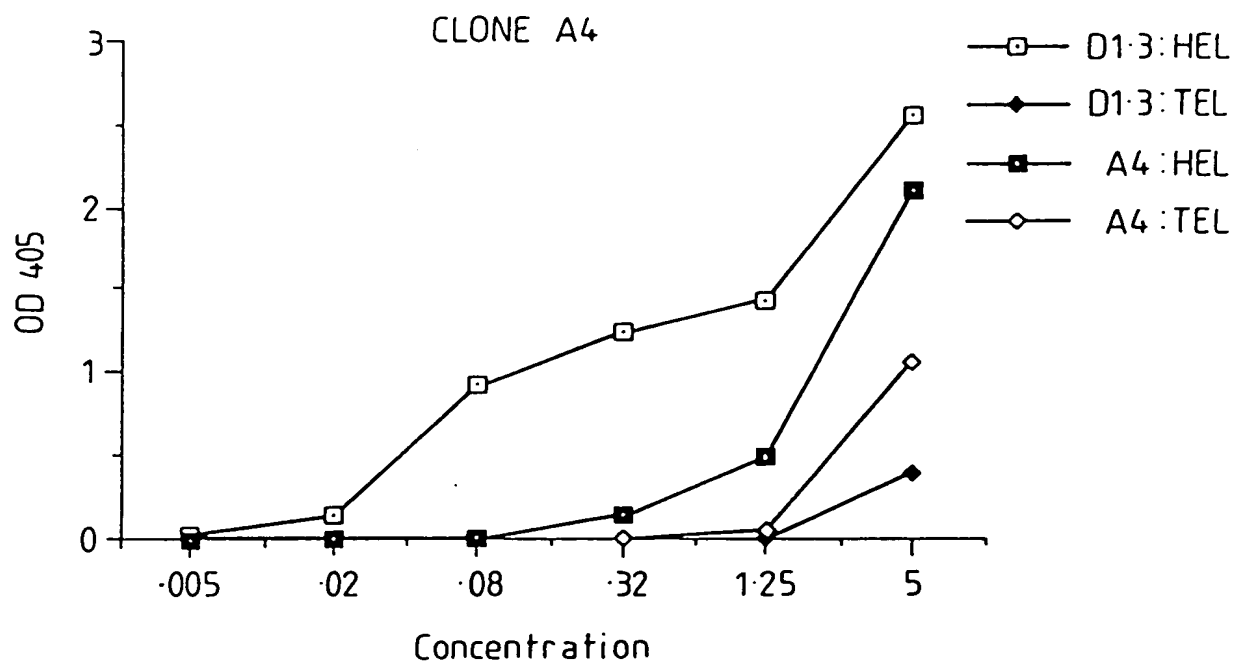


Fig.52.

CDR 1

CDR 2

D1.3 DIQMTQSPASLSASVGETVTITCRASGNIHNYLA WYQQKQKSPQLLVYTTTAD
M1F DIELTQSPSSLSASLGERVSLTCRASQDIGSSLN WLQQEPDGTIKRLIYATSSLDS
M21 DIELTQSPALMAASPGEKVTITCSVSSSISSSNLHWYQQKSETSPKPWIYGTSNLAS

CDR 3

D1.3 GVPSRFSGSGGTQYSLKINSLQPEDFGSYQCQHF^WSTPRTFGGGTKLEIKR
M1F GVPKRFSGSRGSDYSLTISSESEDFVDY^YCLQY^ASSPWTFGGGTKLELKR
M21 GVPVRFSGSGGTSYSLTISSEAE^AATY^YCQ^QWSSYP^LTFGAGTKLEIKR

Fig.51.

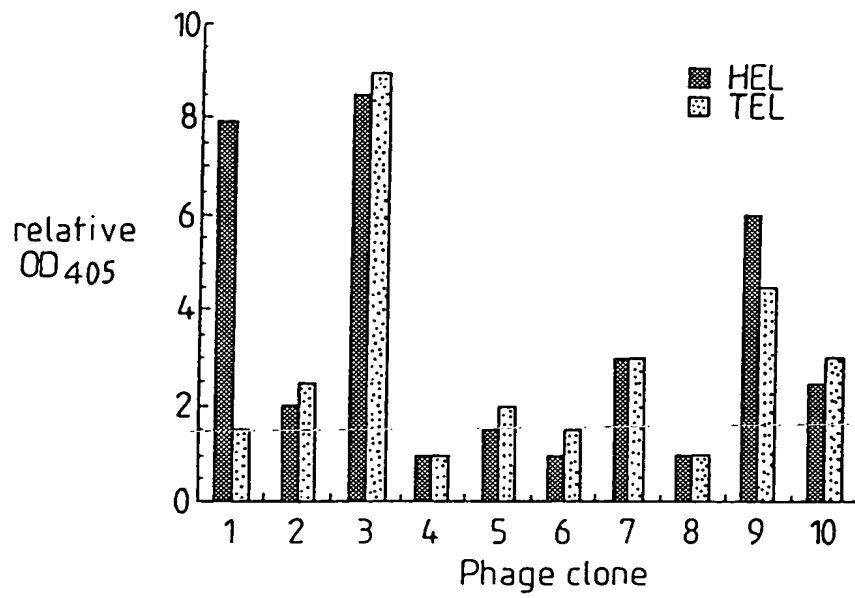


Fig.53.

